

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12396	42764	A	12471	3771	4703	SFOQFCVSFSPSLWFYLLLVFDD GDVQMRFCGCPFCFLVFLTD RTLSCRSVGPICRVRCQCA/LLG GASQLGCSGVKGSRDPLEEAV CPFS/DLQLRAGGNTALFKAVR QGHLSQLRLLSFVCLCPAPRG GAYRGGQASLSCGGLHPV*AS/ RLCLCPKQAWAMAGAPPPASL LAPC/LISDCCASNQSDSVGVGP S/ERPVGVSLSVVRFLSRSEKR NIRGGVTRFSRCRPSPLSLTRK GNSLTPCASQSEGNAGPAGF AHGARTHWALRPVTVHSLCE MNPVPQMEMQKSPVFCVAHA GGCRPEL
12397	42765	A	12472	1	1038	
12398	42766	A	12473	27	428	LADRSAIPGFAFAVTFLLALVG AVLYLYPWTLKPC*SHY*GIN LVVAV*VKTT*GKNCMKMV*L IL*RVTLPS*RFGLRLEKAF*M GHLIKT*LGKNNMKMPCSNWS LF*GTS*KNEKEGTSVNIFSLTP
12399	42767	A	12474	107	362	NKPCFEFYLAALIYLLYHGRK KADTKIPP*ISRFLLIYPSHELTI FIVIHIMCDLGCTWAICFLTISE EVQKKLYEENQVFG
12400	42768	A	12475	193	637	TSSEVVKKQIAQVHNFVIMQL ARENILSS/EDLLVIKVPVLY*GV NENMLTEVPFSFFYDVP*NRL QLHEGIFILFFPSHFVFIK*PI*KAF SNLRPNCAMILLEANDFLIIFKC TTHYHLCNRLHSTKTKHMLAEG HVLGLVWVGEPFI
12401	42769	A	12476	1	1930	
12402	42770	A	12477	1	362	
12403	42771	A	12478	58	160	GVSLQSTSEEGRMRQE*TERE IKVTCRSHYRLA
12404	42772	A	12479	3	410	
12405	42773	A	12480	1	807	
12406	42774	A	12481	154	375	
12407	42775	A	12482	2	512	
12408	42776	C	12483	29	455	
12409	42777	A	12484	209	433	
12410	42778	A	12485	1	1546	
12411	42779	A	12486	3	931	
12412	42780	A	12487	1	363	
12413	42781	A	12488	1	351	
12414	42782	B	12489	82	263	
12415	42783	A	12490	1	1878	
12416	42784	A	12491	24	242	
12417	42785	A	12492	1	3558	

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12418	42786	A	12493	2	478	HNSLSKSDENKENSFSADHVTTA VEKSKESQVTADDEEEKAKA ELIMDDDRVTVDPLLSKSQSILIS TSATASSKKTIEDRNKIKKKSTN NRASSASARLMTSEFLKKSSSK RRTPSTTTSSHYLGLTKVLDQK PFTEEA*EPDRADNIRGSCLFR
12419	42787	A	12494	1	1047	
12420	42788	A	12495	1	1055	
12421	42789	A	12496	212	611	
12422	42790	A	12497	2	195	YVMGRNDGGYLMIDSKTAEIK FVKNNMRDSTFVNKTITAEVL AIDRYSGKNCLLSISWYICG
12423	42791	A	12498	1	429	
12424	42792	A	12499	1	503	
12425	42793	A	12500	3	825	GTTKWQTVRRQKREWIKFAAA CREGEDNSKRNPAAK*SDLQNS LLPALY*KHURSDCESNQKITY RISGVGIDRPPYGVFTINPRTGEI NITSVVDREITPLFLIYCRALNS RGEDLERPLELRVKVMDINDN APVFSQSVYTASIEENSADNTL VVKLCATDADEENHLNSKIAY KIVSQEPGAPMFILNRYTGEV CTMSSFLDREQHSMYNLVVRG SDRDGAADGLSSECDRIKVL VNDNFPT/FRENFKQNSRFSNS LLSSFDQWRKL
12426	42794	A	12501	986	4030	KQRLTWTFSPGKSETMMGLFP RTTGALAIFFVVILVHGLRIET KGQYDEEEMTMQQAQRQKR EWWKFAKPCREGEDNSKRNPAA KITSQYQATQKITYRISGVGIDQ PPFGIFVVDKNTGDINITAIVDR EETPSFLITCRALNAQGLDVEKP LILTVKILDINDNPPVFSQQIFM GEIEENSASNSLVMLNATDAD EPNHLNSKIAFKIVSQEPAGTGM FLLSRNTGEVRLTNSLDRQA SSYRLVVSGA
12427	42795	B	12502	1	3572	
12428	42796	A	12503	1	594	
12429	42797	A	12504	1	612	
12430	42798	B	12505	200	532	
12431	42799	A	12506	2	735	
12432	42800	A	12507	5	400	

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12433	42801	A	12508	2	1260	GQAASPASPASPAMAWAA LLGLLVALLLLLLSRRTTRP GEPPLDLGSIPWLGALDFGKD AASFLLTRMKEKHGDIITLVGG RYVTVLLDPHSYDAVWVEPT RLDFHAYAIFLMERIFDVQLPH YSPSDEKARMKLTLLHRELQAL TEAMYTNLHAVLLGDATAGS GWHMGLLD/CLQLPAQSRLP DSLRN*GAATHP*KPGPGPRPLS *CLPHLSPARPAAPQTGPWLPV SGGQGPVVCQKSPVEAIPSQ AGQAGPPEQMAGELPAAPGGD GCVRGDAGTGPAAA VGHTGE YGSRCLLAPALPSQES*SPGCCP RRAREYPLASGAACLDHDSPT EGSRQHTC/DLIAC*VRASGLQL PPSSPARL/GGPGHAHGRERIQ PATW*PPPPLPPEPPERPRNLH RPRGI
12434	42802	A	12509	3	466	
12435	42803	A	12510	1	1134	
12436	42804	A	12511	2	1211	
12437	42805	A	12512	2	405	HEMLLASEIKHLPRLLIGQERE TQTSELKIKRRGNEEAPS/PPSS AYERGTRPDDRYDTPTSKKK VRIKDRNKLSTEERRKLFEQEV AQREAOQKQQQMQLNGMTSP LPYDSLGYNAPHHFAGYPPGY PMQA
12438	42806	A	12513	191	898	
12439	42807	A	12514	1	270	
12440	42808	A	12515	2	1328	
12441	42809	A	12516	1	2868	
12442	42810	A	12517	1	1254	
12443	42811	A	12518	1	576	

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12444	42812	A	12519	1919	3044	HQGPSTPPSWAMSGPPTPLSRE DWHQGPSTPPSWAMSEPT/SSI QGLASGAVHTJLLGDVRATYTS IQGVTSQVSVQSRRAAQMAVPSS RILQLSKPKAPATLLEWDPVP KPKPHVSDHNRLHLAKVPRK EGSGKKVGAFPEIKGPEAFRDK ARAMESQSNMDMPFDELLALYG YEASDPISDRESEGGVDVDPNLP DMTLDKQIAKDLLSGEEEEET QSSADDLTFSVTSHEASDLFPN RSGCLLAGAEASSRGLLPRAQP VPRGAGLADNSRGALLRAHGT VRVGTATVVKPADAPPESPRDR RSRNDSHRPTGPSESERQPQSN QPTLLLRGHGTIRVVRTATVVKP ADAPAESPRDRSRNDSHGQSS
12445	42813	A	12520	413	1412	
12446	42814	A	12521	293	412	NHLSVAGNGSSPCGL*AGALGL LLWLLASSGHRVLSGMI
12447	42815	A	12522	2	181	
12448	42816	A	12523	1	277	
12449	42817	A	12524	1	739	
12450	42818	A	12525	1	326	
12451	42819	A	12526	3	566	
12452	42820	A	12527	1	465	
12453	42821	A	12528	1	1167	
12454	42822	A	12529	260	395	EVATATPTLSNHYPDQSAAIN/D QG*PLHQKQDHLKQAQMNISIF
12455	42823	A	12530	209	958	FRCVLISFWSHKLHLWYHEGRI VPSDRIVPPHGI/VSSHGVALPQR ILMRQFTLLEGLNKDGRFLIQLS GTAPWSSYFNSVAKFGVIHRIH SFFLSHNGHKAVALDLLSNVG GSCLCGDASSFTTPSRITMTSK SWLARSVAEMSYR/WTALVNH VADDQRGHQKNVIALDWVINR NVQLVNRNHLPRFCSCFLDHLD AHRGTNDHAFQVTHSEHAQ LAISDGNHSMMAENQSFPCPSVS LSCFHENAA
12456	42824	A	12531	1	1965	
12457	42825	C	12532	520	684	

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12458	42826	A	12533	701	1307	GRHLTTNHTAAVVFPPFRPLCS SFFRYSGRFVGAVAGATASGRGQG PAG*DNCQRAWRGAFYKFQAT LSAGAGTRAEEGSDGDGEAAE PGAGTAREPARLRGVSRRFVL DGRRCCLCYFKNPHDPLPLGHL DIAEACFSYQRADEAAEQPAHF QVRSAGAATVLEVGTRALRGV HLIRAHRGIAQWSPVSFLQ AVLPAWLL
12459	42827	A	12534	1	1356	
12460	42828	B	12535	1	1449	
12461	42829	A	12536	3	2449	
12462	42830	A	12537	1	3327	
12463	42831	A	12538	1	1359	
12464	42832	A	12539	1	672	
12465	42833	A	12540	1	1281	
12466	42834	A	12541	1	399	
12467	42835	A	12542	1	399	
12468	42836	A	12543	171	426	PVSCATGEEEDNVLPFKGDDLP R**PGKLWCEFHASSISQALGQ HPRRSVLDTQDSHVLVRRKTT CFSQRAMISPDDDPSQEAGALS RNNLLAPYSALTFMENGNCLL QLFQLGKLLVQASHLHGQLLV FVQKIIISM
12469	42837	A	12544	1	988	
12470	42838	A	12545	3	129	LFHPCQDSQHH*CVCCRLTGH GAA*VHGPGCAVQTYRASH
12471	42839	C	12546	532	1101	
12472	42840	A	12547	197	355	
12473	42841	A	12548	1	1275	
12474	42842	A	12549	3	131	

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12475	42843	A	12550	1746	3504	ESDPSNSTTSM DRTLL/MSSIVP RLPSACRILPTGTIPE*SCVHRT ASLIPLPPGSRKYSPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTSPDISHQQA AALLRTY LKNLSPIYNSTPIFGPLTTQTTI PVAAAPLCISWQRP TGIPLGNLSP SRCSFTLHLRSP TTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCLSLHPWLS SPSSDSDP PRPSSCLLIPSPENNSERLLVDT RRFLIHHENRTFPSTQLPHQSPL QPLTAAALAGSLGVVWQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAGISTSM TFRSLSNDFS ASITDISQTL SVLQAQVDSLAA VVVLQGGRLGLDLLTAEKGGLCI FLNEECFFYLNQSGLVYDNIKK LKDRQAQLANQASNYAESPWA LSNWMSWVLPVPSLPIPIFLLLL FGPCIFRLVSQFIQNRQAITNHS IRQMFLLTSPQYHPLPQDLPSA
12476	42844	A	12551	2	394	
12477	42845	A	12552	1	882	
12478	42846	A	12553	45	409	
12479	42847	A	12554	1	1035	
12480	42848	A	12555	118	312	
12481	42849	A	12556	1	1083	
12482	42850	B	12557	1	1122	
12483	42851	A	12558	97	439	
12484	42852	A	12559	1	450	
12485	42853	A	12560	1	471	

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12486	42854	A	12561	2	1407	WGKNRAEKLETLSRVPLLLQ RNAVPHQQWNKAGRRMTLS* EKKASDD/PNYSKLQEEIQTGK KEVKHFEKNLDECITRITNREK CLKELMELKAKARELREECRL RSQCDQLEERVSVMEIEIQTIRE YYKHL YENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPIGTSE IVAHNSLPTKKSPGPDGFTAKF YQRYKEELIPLLKLFQSEIEKEGI LPNSFYEA SIIIPKQGRDITTKK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQ WFNICKSRNVJHHNRTKDKNH MIISIDAEKAFDKIQPFMLKTL NKLGI DETYLIKIRAIYDKPTAN IILNGQKLEAFPLKTGTQRGGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLFELISNFSKVSGY KINVQISQAFLYTNYRQSAKS
12487	42855	A	12562	1	846	
12488	42856	A	12563	1	1281	
12489	42857	B	12564	1	274	
12490	42858	B	12565	1	2265	
12491	42859	A	12566	1	2742	
12492	42860	A	12567	1	1272	

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12493	42861	A	12568	222	2130	RKKNNKKK*TKPPRNMGLEKRT KMSDWCCT*K*GEWNQV/AK TLCRILSRRT/YPNLRQADIQIQ EIQRTPQRYSSRRATPKHIIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLTADLSAETLQARRE WGQIFNII.KEKNFQPRISYPAKL SFISEGEIKPFTDKQMLRDFVTT RPALKELKKEVLNEMERNRKK LNRPTIGSEIVAIINSLPTKKSPG PDGFTAEFYQRYKEELVPFLLK LFQSKEKEGIIHNSFDEASIIIP KAGRDTTCKDNFRPISLMNIDA KILNKILANQIQHIKLIHHDDQ VGFIQMGQGWFNICQSNVIQHI NRTKDKNHVVISIDAEKAFDQIQ QRFMLKTLNKLIDRMYLKIIIR AIYDKPTANILNGQKLEAFPLK MGTTRQGCPLSPLFNIVLEVLA RAIRQEKIKHIIQLGKKEVILSL FADDMIVYLENSIVSAQNLLKLI SNFSKVSQYKINQKSHALFHT NNRQTESQIMSELPFTIASKRIK YLGIIQLTKDVKDLFKENYKPLL NEIKEDTKKWKHIPCWSVWGRIN IVKMAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRAHT AKSILSQKNKAGGITLPDFQLY CKATVTKTAWY
12494	42862	A	12569	1	474	
12495	42863	A	12570	1	1197	
12496	42864	A	12571	1	1518	
12497	42865	A	12572	1	3189	
12498	42866	A	12573	1	2199	
12499	42867	A	12574	3	2820	ENKDTTYQNLWDAFKAVCRG KFIALNAHKKRQERSKIDTLTS QLKELEKQEQTHSKASRRQET KIRAEKKEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKKREK NQIDTIKNDKGDITDPTETIQT REYYKHLYANKLKNLEEMDKF LDITYLPRLNQEEVESLNRPIITG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIIIPKGRDITTK KENFR
12500	42868	B	12575	1	1593	

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12501	42869	A	12576	1	3549	MGDFNTPLSTLDRSRRQKVNK DTQELNSALHQVDLIDYRTLH HKSTEYTFPSAPHHTYISKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQNRSTTWKLN NLLNDYWIHNKMKAEIKMFF ETNKNKDDTTYQNLWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQ EVTKIRAEKKEIETQKTLQKINE SRSWFFERINKIDRMLARLIKK KREKNQIDTIKNDK
12502	42870	A	12577	1	2724	
12503	42871	A	12578	1	3567	
12504	42872	B	12579	709	2064	
12505	42873	A	12580	1	3370	
12506	42874	A	12581	1	2024	MGFYHVGQAGTELLTSNDPLT SASQSARITGKALQKPTVPVP YEKMLQDQSALIVQGLPEGVA FKHPENYDLATLKWILENTAGI SFIINSATIEPPAAQPMSTHMG HSLCVLVVETHAKPVAVQSSSF TRNPEVISLEVAAVTVKEESD PDYDYITFKDLPGLIAYETKAYV LWPQLSKICKSNGDKNKAYRG QQCRLRQQNPLAALTGKISVSV YVSHPSLSRSVIGWTRQVARQT MQKDRDGPLKNEGECNCAGSE KNTLTSQLEKEKQEQTHSKAS RRQEITKIRAEKKEIETQKTVEK INESRSWFFERINKIDRPLARLIK KKREKNQVDAIKNDKGDITDP TEIQTTHREYYKHLAYANKLENV EEMDKFLDITYTLPRLNQEEVES LNRPIITGSEIVAINSLPTKKSPG PDGFTAIFYQRYKEELVPFLK LFQSIKEGILPNSFYEASIIIAK PGRDITTKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSNVIQHIN RAKDKKHMIISIDAEKAFDKIQ QPFMLKSLNKL/DIGKNYFKVH MGPKKSPCRQVNPKEQSWR HHST* ¹ LQTLQGYSNQNSMVLV PKQRYRSMQNTALRNATYL QLSDL* ² QT* ³ EKQAMGKGFI**
12507	42875	A	12582	722	4214	

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12508	42876	A	12583	228	1152	KNRDYKNLSLRPQCNRQTQON *ESHKPLNYMETEQPAPE*LL DT*RMKAEIKMFFETNENKDT TYQNLWDAFKATASKTNKEKE KNQIDTIKNDKGDIITDPTIEQT TIREYYKHLKYANKLENLEEMD KFLDTYTLPRNLQEEVESLNRPI TGAIEVAIINSLPTKKSPGPDGF TAEFYQRYKEELIGWLRRESVSK ICLKFDHQVQVITGRLIIRFQIAF GTVVLCQLTRHIDVVFVGKRLA NARFAPSLGGAPDLFTLKPCFV AVETQGDLPQATTVDIDGCL GKPANVQVALDLDVKGFGQQW
12509	42877	A	12584	1	2028	
12510	42878	A	12585	2	2264	
12511	42879	A	12586	1	2130	
12512	42880	A	12587	1	2900	MENDFDELREEGFRQSNYSER EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELTKAQELR EEWRSLRSRCDQLEERVSAME DEMNMKGEGKFKREKRIKRN QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLTYN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPIITGAE
12513	42881	A	12588	1	2745	
12514	42882	B	12589	1	3288	
12515	42883	A	12590	1090	2526	
12516	42884	A	12591	1	3242	
12517	42885	A	12592	3862	8976	RAKSPANIIMTGSNSHITILTN VNLNSPIKRRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFPSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSHSAIKL ELRIKNLTQSR
12518	42886	A	12593	1	1000	

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12519	42887	A	12594	1	979	MNNAKENFLGRFDGRIGTAP VYSPQHQRRRRVISALPTEPPL VIPRQTGFQVDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGRRQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRLQVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDL KTMARELRDSCSFQRQDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIRQEKEIKGQL GKEEVKLSLFADNMTVYLENPI IS/PKISLS**ATSAKSDIKSMC KNHKHSYTPITDKQRAKS
12520	42888	A	12595	1140	2210	KPWHKFNFTHAQASADLIKW KKGYQ*LKIKLMK*SKKTRNTN YHQNTINISMQIN*KI*KKWRNS WTHTLQY*TRKLLNLIDQ*Q ALKL/QAIIYSLPTKNVQGMQD SQSNTRTVWGILARAIQKEI KDIQLENEEVKLSLFADDMTVY LENSIVSAQNLLKRLIKYLGIL TTDVKDLFKENYKPLLNIKED TNKWKNIPCSIRGINIMKMAI LPKLIYRFNAIPKLPMTFFTELE KATLKFIVNQKRAHIAKTILSK KNKAGGIMLPDFKLYYKATAT KAAWYWYQNRDIDKLTQIYK KKTNNPIKKWAKDMNRHLSKE DIYGANRHMKKCSSSLVIREKQ IKTTMR
12521	42889	A	12596	520	697	GLCSVPLLCISVLVPVPCFCGYC SLVV*FEVR*SDASSFVLLA*DF LGNVSVFLVPYEL
12522	42890	A	12597	1	1410	
12523	42891	A	12598	1	1461	
12524	42892	A	12599	77	457	QALKLRQ*LIAYQPKRVQDQM DSQTSNARGTKRSWYHSF*NYS N/PTEKEGILLNSFYEAQIILPKP GRDITTKKENFRPISLMSINAKIL NKILANRILQHIKKLNTIKSASS LGCKAGSTYANQ

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12525	42893	A	12600	1	919	MGDFNTPLSTLDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNCSTTWKLN MLLNDYWEHNKMKAEIKMFF ETNKNKDDTYQNLWDTLKAVC RGKFKALNAHKRKKERSQIDTL TSQLEKEKQEQTSHKASRRQE ITKIRAELEKETETQKTLQRLMN PGAVLEVLAARIRQEKEIKGIQL GKEEVKLSLFADDMMIVYLENP MSQPKISLS**ATSAKSQDIKSIY KNHQHSYTPIRDQKRAKS
12526	42894	A	12601	1	1264	MDKFLDTYTLRLNQEEVESLN RPTGSEIEAINSLPTQKSSGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIIIPKPG RYTHKKNNFRPISLMNIDAKIL NKILANRIQQHHKKLIHQDQVGI IPGMQSWFNHKSINVIQHINRT KDKNHMIIISIDAFAFDKIQPF MLKTLNKLKIPKNPTYKGCE GPLQGELEQITAQNRKGRHKQM EEHPMLMDRKNEYHKNNGHTPK VIYRFNVIPKLPMTFFSELEKST LKFIWNQKRARIATILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEM TPHIYNHLIFDKPDKNKQWGW DSLFNKWCWENWLAIGRQLKL DPFLTPYTKINSRWIKDLNVRP KTIKLEENLGNTIQDISMGKDF MSKTPKAMATKAKMDKWDLI KLKSFACTAKETTIRQSWPEMTK FTFSNTDVKNWKGKNNIGR HKTSVNTCKMDSGLVLERWM EWNPGFPLSIDAKCHKDLPRDI QFDSEKGVDFVLNYSKANMR WAGSMFL*FIESF*HEWLLNFV KGLFCIY*DNHVVVFVGSYYML
12527	42895	B	12602	1	1827	
12528	42896	B	12603	13	1377	
12529	42897	A	12604	557	664	KTPLSQPKISLS**ATTAKSQDT KSVYKNQQHSYT

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12530	42898	A	12605	77	1866	QAPKLRQ*LIAYQPKKVQDQTD SQPNSTRGTTKSWYHSF*NFSN/ PIEKEGIFPNLFYEANILIPKPGR DTTKKENFRPISLMNVNAKILN KLLANQIQQHKKLIHHNVQVFI PGMQGWFNICKSINVIQHINRT KDKNHRSSISIDAEKAFNKIQPF MLKTLNKLDDMIYVLENPIVSA KNLLKLISNFSKVSQYKINVQK SQAFLYTNNRQAESQIMSASF TIASKRIKYLGLQTRDVKDLFK ENYKPVNLNKIKEDTNKWKNI LWIGRVNIMKMAILPKVIYRFN APIKLPMTFFTELEKTTLKFIW NQKRAHIAKTILSKKNKAGGIT LPDFKLYYKATVTKTAWHWY QNRDIDQWNRTEPSEIPIHYNH LIFDKLDKNKTLGKDYLFNKRC WENWLAICRKLKLDPLTRYT KINSRWIKDLNIRPKTIKLEEN LGDITQDIGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWENIFAIPYSDK GLISRIYKELKQIYKKSSNNPIK KWAKDMNRYFSKEDIYAANR HMKKCSSSLALREMQIKTTMR YHLIPVRMAIHKSGNNRCW
12531	42899	A	12606	67	243	GLCCVFLIYISVLVPVPCCFGYC SLVV*FEVR*HDASSFVLA*D* LGDVGSFLVPYEL
12532	42900	A	12607	1554	1692	
12533	42901	A	12608	640	816	GLCSVALVCISVLVPVPCCFGY CSLVV*FEVR*HDASSFVLA*D *LGNVDSLVPYEL
12534	42902	A	12609	1626	1739	

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12535	42903	A	12610	1	2014	MKREGSLEKKRIKRNESLQEI CDYVKRANRLRIGGPESDGENG TKLENTLQDMQEKFPNLRQA NIQIQEIQRTPQRYSSRA IPRHI IVRFTKVEMKEKMLRAAREKG QVTHKGKSIRLTADLSAETLQA RREWGPIFNILKEKNFQPRISYP GKLSFISEGEIKSFDTKQMLRDF VTTTPALKELLKEALNMEKNK QYQPPQKHAKLTREARANTFK PSRRREITKIRAELKEIETPKTAQ KINESRSWFSERINKIDRPLARL RKKKREKNQIDTIKNDGDDIT HPTIHTIIEYYKHLYANKLEN LEEMDKFLDTYTLPRPNQEEVE SLNGPIAGSEIQAIIINSLPTKSP GPDGFYQRYKEELVPFRLLKFQ SIEKEGILPNSFYEAIIIPKPGR DTTKKENFRPISLLNINAKILNKI LANRIQQHIKKLMHHDQVGFIP GMQGWFNIRKSNVQIHINRTK DKNHMIISDAEAKAFDKIQQPF MLKTLNKLGDGTGTHKIJIRANY DKPTANILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAIR QEKETEGIQLGKEEVKLSLFAD DMIVYLENPM SQPKISLS**ATS AKSQDTKSMCKNHKYSYTPIT DKQRAKSSVNSPFTIA SKRIKYL GIQLTRYVKDLFKERSMK
12536	42904	A	12611	1	700	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLSTKKSPGPD GFIAQFYQRTKDKNHMIISDAE KAFDKIQQHFM LKTLNKLGDG TYLKIJIRAVYDKPTASIIINGQK LEAFPLKTGT RQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLGKE EVKLSLFADDMIVYLENPM SQ PKISLS**ANSAKSQDIKSMCKN LKHSYTLITDKQRAKSSVNSHS QLLQRE
12537	42905	A	12613	1	1765	
12538	42906	A	12614	1	2310	

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12539	42907	A	12615	1	836	MENEFDELTEVHFRRWVITNSS ELKEHVLTCCEEAKNLARRNK LENLEEMDKFLATYTFPSLNQE EVESLNRPTSSIEAAINSLPTK KHGPGDGFATAFYQRYKEELHI NRAKDKNHMIIISDAEKAFDKI QHPVKLILNKLGI DGTLYKIIIR AIYDKPTANLILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVL RAIRQEKEIKGIQLGKEEVKLSL FADDRLYI*GTPLSQPKISLS** ATSAKSQDTKSMYKNHSHSYT PTTDKQRAKS
12540	42908	A	12616	355	4502	QSARFRGRRTLRRPGVGYSLVV *FEVR*CDASSFVLLA*DCLGN AGSFLVPYEL
12541	42909	A	12617	248	362	
12542	42910	A	12618	529	680	YYTRCSKWWNCVLP*YIYNF HLPHGKLKNTDYIKKKLHDFFF KNSKHI
12543	42911	A	12619	1	641	
12544	42912	B	12620	36	48	
12545	42913	A	12621	1	326	
12546	42914	A	12622	1	444	PGSTHASAHACERLQTRTLRAF SSQRRFPATASRASLSSNMAKIS SPTETERCIESLIAVFQKYAGKD GYNNTLSKTEFLSFMNTELA TKNQKDPGCP*PHDGRKLGQPT VDGQLDFSEFLNLIGQAMAC HDSFLKAVPSQKRT
12547	42915	A	12623	2	6008	
12548	42916	A	12624	530	856	

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12549	42917	A	12625	1	952	MAARGTGDKVKPGCEEAGAAF ELPPSVYAAALHESHQHQPCPA GGARAQRVPGGIVTEPLCTTP KDMVFLSDDGDDDDDDNDND GGGDDDDNDGNDNDGNDNDGND DDGDDDDNDGDDDDNDNDGND NDGDDNDNDGDDDDNDNDND GGDDDDGVDGDDNDSDGNDG DDDDSDDDGDSNGYDDGDD GNDDDGDDSDDDSDNDGDD NGDGGDDGGGGDDDDNGHDD DGDMMMMIIVMMVMMVMMV MMVMMVMMVVVVQLRKRAEA SVSEAKCSINVSDDNDGDDGND DGDGDDSDGDDDDGGDDGGD SELTNQFPTNHSGMKASKLRK DSDHREW*W**WWWCN*GR EQRPVFLKQSAQLMSVMIMMM VMVMMVMMIIVMMVMMTMV VVMVVIVNSPINSRLITQA
12550	42918	A	12626	3	380	
12551	42919	A	12627	5	765	RQWEVGRWSGTTFISCFCKKTL YFTNPSFSSSLVTVILRREVT CGGAPEQRYQIIPVCVAARLPT RAQDVLDAHLSEVNAVRFPGN SSLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDGDP VRNSAPVAVDCALSDLHTGQG YQVLAATYNQAAQLWKVGEA QSKETLSGHKDKVTAAKFKLT RHQAVTGSRRDRTVKEWDLGRA YSPKRQRPSTGHDDGGFVE KKRGKCGEKRDQIVTVSV
12552	42920	B	12628	1	2802	
12553	42921	A	12629	458	708	QNRHRHHGPFMSVAVSSQLLD TPAERLSLHTWKIAQRPGRGTP HFPDGA/VQAETLPQTGRPR GTPHFPDGAASSFGYCCLVA
12554	42922	A	12630	2300	6491	EGLEALIHQERLSYWANQVSED RPVCKAIQKQFEGLVDTGAD VSIHALNQWPKNWPKQKAVTG LVGIGTASEVYQSMEILHCLGP DNQESTVQPMITSIPLNLWGRD LLQQWGAETMPAPLYSPTSQK IMTKMGYIPGKGLGKNEDGIK VPVEAKINQEREGIGYPFLGAV TVEPPKPIPLTWKTEKPVVWNQ WLPKQKLEALHLLANEQLEK GHIEPSFSPWNSPVFVIQKSKGK WHTLTDLRAVNAV

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12555	42923	A	12631	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDKAKACRSIYPLH DVFVRKVVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
12556	42924	A	12632	1	642	
12557	42925	A	12633	260	534	
12558	42926	A	12634	1	438	
12559	42927	C	12635	391	750	
12560	42928	A	12636	199	451	
12561	42929	A	12637	120	992	RDRIPGPVCKGKWKNERILIFS SRGINFRTRHLMQDLRMLMPH SKVHDTNMARSDNLSVINEGCE MNNWLRCIYFEAKKKQDLYM WLSNSPDGSAKFLVQNIHTLA ELKMTGNCLKGSRPLLSDPAF DELPHYALLKELLIQIFSTPRYH PKSQPFVDHVFTTILDNRIWFR NFQIIEEDAALVEIGPRFVLNLIK IFQGSFGGPTLYENPHYQSPNM HRRVIRISTAAKYREKQVQKDV QKLRKKPEPKTLLPHDPAADV VTPAEKPIEQVVKPETKVDL KASV
12562	42930	A	12638	1	342	
12563	42931	A	12639	1	580	PGWEKMRSS/GVNTQEALPT AAIPTDAKVRVYFNHITNASQ WERPIGNSSSGGKNGQGEPARV RCSHLLVKHSQSRPSSWRQEK ITRTKEEVALELINGYIQIKSGE EDFESLASQSDCSSAKA/RGD LGSFSRGQMOKPF*RTPRFAL RTGGDERGPCFTD/SCIHIILPHL SEGKPRPLGAGQGG
12564	42932	A	12640	3	116	
12565	42933	A	12641	2	253	
12566	42934	A	12642	3	512	EDYLERKQ/VPTCEQTHSKLG GPMTLKREVKP/KVDVSPSKKG PLQHIHTLLVCHVRIFYPGSIQ/ VRWFLNGRKKTAGVVSPLNLR NGDWT/FQILVMLEM/TPQQGD VYTCCQVHTSLDSPVTVEWKA QSDSARSKTLTGAGGFVLGLIIC GVGIFMHRSSKAFNEDLHKQG
12567	42935	A	12643	1	363	
12568	42936	B	12644	70	1229	
12569	42937	A	12645	1	430	
12570	42938	B	12646	1	1321	
12571	42939	A	12647	3	446	

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12572	42940	A	12648	1	417	
12573	42941	A	12649	269	452	TILRSFGYFFRRINIMLTEEKIKS DHRKISQLIFLQKLCQTLQSENV SQGGMLYRAKA*H*T*TLVVW *HVMSPYHKGLMLSLCSVK HSTLRDVFTL
12574	42942	A	12650	83	1385	
12575	42943	A	12651	1	974	MNPLECVDRSSQPWGNPTWTS SGMRSVTLVGVFKLTLFALAQT LNAAASLTGQELLAGFPVGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMKNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLKFANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCIGLQMGNTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGLPPCLGPSQE
12576	42944	A	12652	1	1103	MNPLECVDRSSQPWGNPTWTS SGMRSVTLVGVFKLTLFALAQT LNAAASLTGQELLWNFPLLMF AWKIAPALCCGNTVVIKPAEQT PLSALYMGALIKEAGFPVGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMKNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLKFANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCIGLQMGNTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGLPPCLGPSQE
12577	42945	A	12653	1	729	
12578	42946	A	12654	259	390	SFCSANFEVFRLLTAQQ*FVR*H ALSHIF*G*V*SFPKSTKRVNF
12579	42947	A	12655	68	735	
12580	42948	A	12656	1	825	
12581	42949	A	12657	3	470	
12582	42950	A	12658	1	1683	

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12583	42951	A	12659	1	1748	MNKPPIRNLSENAAPLDLEGIL KDAKIPVSGPFLVKIGYAFVDC PDEIWAALKAEIALSGKIELHGK IEVEHSVPKRQRIKQLQIRNIPPH LQWEVLDS*LVQYGVVESCQ VNTDSETAVVNTYSSKDQAR QALDK/LLDKLNGFLENFTLK VAYIPDEMATQQNPFLQPRGR GLGQRGSSRQSGSPGVSQKPC DLPLCLLVPTQFVGAIGKEGAT IRNITKQTQSKIDVHRKENAGA AEKSITILSTPEGTSAAKSILEI MRKETQDVKFTTEIPLKILAQN NFVRLIGKEGRNLKKIEQD TKITISPLQELMQYNPEHTITAK GNVETCAKAEIEIMKKIRER*E NDITSM/N/LQAHLPGLNLNAL GLFPPTSQMPPTSGPPSAMTPP SPQSEQSESETVHLFIPALSVRA LISKQGGHIKQLSRFAGASSKIA PVEAPDAKVRMVMIAAGSPEAR FKAQGRIGYKIKKEENFVSPKEE VKLEAHIRVPSFAAGRVIGKGG KTVNELQNFSSAEVVPVRDQTP DENDQVVVKITGHFYACQVAQ RKIQEILTQVKQHQQKALQSG
12584	42952	A	12660	3	803	
12585	42953	B	12661	1	330	
12586	42954	C	12662	127	342	
12587	42955	A	12663	324	491	
12588	42956	A	12664	1	891	
12589	42957	B	12665	1	1869	
12590	42958	A	12666	2	136	
12591	42959	A	12667	108	355	
12592	42960	A	12668	2	811	FGMRGSRGGWAGEMAASGES GTSGGGSTEEAFMTFYSEVKQ IEKRDSVLTSKNQIERLTRPGSS YFNLNPFVELQIDPEVTDIEIKK RFRQLSILVHPDKNQDDADRA\ QKAFAEAVDKAYKLLDQEQKK RALDVIQAGKEYVEHTVKERK KQLKKEGKPTIVEEDDPFLFKQ AVYKQTMKLF AELEIKRKERE AKEMHERKKRQREEEIEAQEKA KR/EEREWQKNFEESRDGRVD SWRNFQAQFRRKKEKKNRTE LRPESKNGSNVE
12593	42961	A	12669	731	850	
12594	42962	A	12670	201	377	LMTLPCKIPSPGSSWLKISPIEHL MTPTPASQRTTPDCNFPLPTQI L*NGPTPISLH

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12595	42963	A	12671	742	2982	KIPFFDASFLPCLHKFNLKGGKNSKGFKMAEKFESLMNIHGFDLGSRVMDLKLPGCGGNGLVFSAVDNDCDKRVAIKKIVLTDPSVKHALREIKIRRLDHDNIVKVFEILGPSGSQLTDDVGSLETLSNVYIVQEYMETDLANVLEQGPLLEEHARLFMYQLLRGLKYIHSANVLHRDLKPANLFINTEDLVLKI GDFGLARJMDPHYSHKGHLSEGLVTKWYRSPRLLLSPNNYTKAIDMWAAGCIFAEMLTGKTLFAGAHELEQMQLILESIPVVHEEDRQELLSPVPIRNDMTEPHKPLTQLLPGISREALDFLEQLTFSFMDRLTAEALSHPYMSIYSFPMDEPISSHPFHIEDEVDDILLMDETHSHIYNWERYHDCQFSEHDWPVHNNFDIDEVQLDPRALSDVTDEEEVQVDPRKYLDGDREKYLEDPAFDTNYSTPCWQYSDHHENKYCDLECSHTCNYKTRS SSYLDNLVWRESEVNHYEYEPKLIIDL SNWKEQSKEKSDKKGKSKCERNGLVKAQIALEEASQQLAGKERENQGFDFDSFIAGTJHL\SSQHEPTDVGDKLNDLNSSVSQLELKSLSKSVSQEKQEKGMANLAQLEALYQSSWDSQFVSGGEDCFFINQFCEVRKDEQVEKEN TYTSYLDKFFSRKEDTEMLETEPVEDGKLGERGHEEGFLNNSGE
12596	42964	A	12672	826	1041	WKITVKGGVFLWWAGVGDTKVLSSGGA*ARMSQEEDFHKVMSSVKARTGHLHFFCGGMSSVKAGQGPFSVLL
12597	42965	A	12673	1	1482	
12598	42966	A	12674	3	488	
12599	42967	A	12675	2	114	

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12600	42968	A	12676	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSTIRRIIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSSDFCHWGQRFR Y\SYIDESQGEIY* SIEHLDKMG MSIIEQLDPVSFSNYLKKYHN TICGRHPIGVLLNAITELQKNGM NMSFS\FLNYAQSSQCARNWQD SSVSYAAGALT TVH
12601	42969	A	12677	2	114	
12602	42970	A	12678	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSTIRRIIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSSDFCHWGQRFR Y\SYIDESQGEIY* SIEHLDKMG MSIIEQLDPVSFSNYLKKYHN TICGRHPIGVLLNAITELQKNGM NMSFS\FLNYAQSSQCARNWQD SSVSYAAGALT TVH
12603	42971	A	12679	1	912	
12604	42972	A	12680	1	156	
12605	42973	A	12681	112	1120	
12606	42974	A	12682	33	415	NMNKPIPTSTYVRCLNVGLIRK LSDFDIDPQEGWKLAVAIKKPS GDDRYNQFHIIDAVPKTANTLP SKEAITVQKQMPFCDKDRTL MTPVQNLEQSYMPDSSSPENK SLEVSDFRHSFSFYELKN
12607	42975	A	12683	3	311	
12608	42976	A	12684	1	1125	
12609	42977	A	12685	1	1365	
12610	42978	A	12686	3	141	VVSTVVPDS/AHKLFIGGLPNYL NDDQCHGLSKGAFCEYVDIN VT

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12611	42979	A	12687	1	1255	GTRSTSSLRRQMKNIHVHNYSEA EIKVREATSNDPWGPSSSLMSEI ADLTYNVVAFSEIMSIWKRL NDHGKNWRHVYKAMTLMLEYL IKTGSERVQQCKENMYAVQT LKDFQYVDRDGKDQGVNVRE KAKQLVALLRDEDLREERAH ALKTKKLAQTATASSAAGVS GPPPEAEQAWPQSSGEEELQLQ LALAMSKEEADQEERIRRGDDL RARRWQSRARRGRLGARRSRPS WTLTSSRPQLLPRPQTPGGAQ HPWLLPSPRLPPRTPGAAPLSL QLLIPGEVQPPRRPLGTPGGLLP LQDPQLTLGVGPQLQLGRGPR LIHGEVPMVGSRSVGPQPPIGH RPRPSQIPGEGHLPSPAPMAQQ QPGDSTRSPTSSLTLTDSARHCR PPGAAQESWSCWQERCRPEAL
12612	42980	A	12688	116	1541	
12613	42981	A	12689	3	415	
12614	42982	A	12690	1	1440	
12615	42983	C	12691	117	314	
12616	42984	A	12692	3	120	
12617	42985	A	12693	1	729	
12618	42986	A	12694	79	870	EWSSVRRSLVEKRALRRPHPQC LCFRMKTILSNQTCRPFPEINVD ITLKGRAVIV*GPAEGTLR\RDF \NHLQW*NLSLSWKEKKRGRS VDK\WWGNRKGNWPT\VRTYL VVHVQNMIKGVLPGLPVTKD EGLVYA\HFPHPTLVIPGRNGSS LLKSRNFLGVKNTSRRVSG*RP G\VACS\VSSSPRKDEFNPLKGN DIGACFQISAGFGFQQAPTHCL KTRDIQGNFWDGYPMVLWKK GTVSARAGWNKDLKEFTWATE RKMPG
12619	42987	A	12695	2	293	
12620	42988	A	12696	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPKIVTLAT LKMS
12621	42989	A	12697	1	1308	

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12622	42990	A	12698	124	1135	DKNSMGLPGVIPSAAVLSWSI HLSSALSPITISACRHPMEDSM DMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTV SLGAGAKDELHIVEAEAMNVE GSPKIVTLATLKMSVQPTVSLG GFEITPPVVLRLKCGSGPVHISG QHLVAVEEDAEESEEEEEVK\ LLSISGKRSAPGGGSKVPQKK\ KLAAD\EDDDDDDEEDDDDD \DDDDFDDEEAEEKAPVK\KSI\ RDTPAKNAQKSNQNGKDSKPS STPRSKGQESFKKQEKTPKPK GPSSVEDIKAKMQASIA/EKGG LPKVEAKFINYVKNCFRMTDQ EATQDLWQWRKSL
12623	42991	A	12699	201	416	
12624	42992	A	12700	2	678	
12625	42993	A	12701	3	2149	
12626	42994	A	12702	1	219	
12627	42995	A	12704	267	437	
12628	42996	A	12705	507	845	
12629	42997	A	12706	426	704	SRRWGGVHSCPPSPPTAGHWT LLILCAKARRSEAAAMVLASRRR RPGPRPRRRRLPVLGSRGGAG PARGRGPGSGWGPLRAAPSP*P SSTV
12630	42998	A	12707	195	892	
12631	42999	A	12708	1	893	
12632	43000	A	12709	1	777	
12633	43001	A	12710	1	439	KTQVAPSTDGIQIP\SSNSRTDE REFFIASYNRKKEDEGEGNVWIA KSSAGAKGEGILISSEASELLDFI DNQAQVHVQKYLEHPLLLPEPG HRKFDIRSWVLVDHQYNIYLY REGVLRTASEPYHVDNFQDKT CHLTNHCQKQKKKK
12634	43002	A	12711	1	394	SGTRPVFLVPHTIGIPHPAIVTP QVKQEHPHTDSDLMHVVKPQHE QRKEQEPKRPKHPKPLNAFMLY MKEMRANVVAECTLKESAAIN QILGRRWHALSREEQAKYYEL ARKERQLHMQLYPGWSARDN
12635	43003	A	12712	1	789	
12636	43004	A	12713	1	870	
12637	43005	A	12714	1	729	
12638	43006	A	12715	1	828	
12639	43007	A	12716	1	213	
12640	43008	A	12717	1	664	
12641	43009	A	12718	1	695	
12642	43010	A	12719	96	269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
12643	43011	A	12720	3	241	
12644	43012	A	12721	213	660	EGPARHRLSPVRSKMTKKR RNNGRAQKRAARHVRGPSPLK/ CFPSGLPPNCAICVCPKDKAIK KFFVVRNIVEAAAR/DISEASV FDAYL/LPKL/YVKLHV/CVSCAI HKQK*SGNRSS*SPAKTRTPPR FR/PGG*LPHGPPTKSP
12645	43013	A	12722	1	303	
12646	43014	A	12723	610	928	FLSLPTFLFV/IFSGEELLVLALV FLSLFFFFFFLRWSEFVVAQAV/ VQW/INLSSLPFGKQFSCLSLP SSWDYRCPPPRPANCFITRDG VSPCCPGWSRTSDLR
12647	43015	A	12724	1	2775	
12648	43016	A	12725	1	6039	
12649	43017	A	12726	2	3661	
12650	43018	A	12727	1	1173	
12651	43019	A	12728	1	1632	MPNPKNSKGGRKNKRANSSGD EQENGAGALAAAGAAAGAAAG GALAAAGCGAAAAGAPGAG GAAGAGGAGTGAANAAAAAG AAAAGDAKNEAPCATPLCSFG RPVDLEKDDYQKVVCNNEHC PCSTWMHLQCFYEWESSILVQF NCIGRARTWNEKQCRQNMWT KKGYDL/AFRCSCRCGQGNL KKDTDWYQVKRMQDEKKKKS GSEKNTGRPPGEAAEEAKCRP PNKPQKGPSHDLPRRHSMDRQ NSQEKA V GAAAYGARSPGGSP GQSPPTGYSILSPAHSFGRSSR YLGEFLKNAIHLPEHKKAMAG GHVFRNAHFDYSPAGLAVHRG GHFDTPVQFLRRDLSELLTHIP RHKLNTFHVVRMEDDAQVQGG EDLRKFILAAALSASHRNVNCA LCHRALPVFEQFLVDGTLFLSP SRHDEIYDVPCHLQGRMLHL YAVCVDCLEGVHKIICICKSR WDGSHWQLGTMYYDILAASP CCQARLNCKHCGKPVIDVRIG MQYFSEYSNVQCPHCGNLDY HFVKPFSSFKVLEAY
12652	43020	A	12729	1	1485	
12653	43021	A	12730	1	1074	
12654	43022	A	12731	2	3394	
12655	43023	A	12732	1	2190	
12656	43024	A	12733	1	1251	
12657	43025	A	12734	1	1710	
12658	43026	A	12735	3	679	

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12659	43027	A	12736	209	337	
12660	43028	A	12737	365	538	
12661	43029	A	12738	2	196	
12662	43030	A	12739	1	2639	
12663	43031	A	12740	3	173	
12664	43032	A	12741	1	1479	
12665	43033	A	12742	1	921	
12666	43034	A	12743	1	798	
12667	43035	A	12744	2	773	
12668	43036	B	12745	75	321	
12669	43037	A	12746	321	738	
12670	43038	A	12747	1	3190	
12671	43039	A	12748	287	1636	ACGAMERAPPDGPLNASGALA GDAAGGARGGSAAWTAVL AALMALIVATVIGNALVMLA FVADSSLRTQNNFFLLNLAISDF LVGAFCIPLYVPYVLTGRWTFG RGLCKLWLVVDYLLCTSSAFNI VLISYDRFLSVTRAVSYRAQQG DTRRAVRKMLLVVWVLAFLLYG PAISWEYLSGGSSIPEGHCHYAE FFYNWYFLITASTLEFFTPFLSV TFNLSIYLNIGRRTRLRLDGR EAAGPEPPPEAQSPPPPGCWG CWQKGHGHEAMPLHRYGVGEA AVGAEAGEATLGGGGGGGSA SPTSSSGSSRGTERPRSLKRG KPSASSASLEKRMKMVSQSFTQ RFRLAIRDREKESLAVIVSIFG LCWAPYTLMIIRAACHGHCV DYWYETSFVLLWANSVNPV LYPLCHHSFRRAFTKLLCPQKL KIQPHSSLEHCWK
12672	43040	A	12749	1	2142	
12673	43041	A	12750	3	711	VWVNSDLMVINRSTTELPLTV SYDKVSLGRLRFVWHMQDAVY SLQQGFSEKDADEVKGFVDT NLYFLALTFVAAFHLLFDFLA FKNDISFVKKKSMIGMSTKA VLWRCFSTVVFLLDEQTSLL VLVPAGVW/AAIELWES*/RK/ VI*RWTFVWGLMPEFQGTYS ESERKTEEYDTQAMKYLSYLL YPLCVGGAVYSLNLIKYSWY SWLNSFVNGVYAFGLFMLPQ
12674	43042	A	12751	1	2025	
12675	43043	A	12752	494	747	ATVKWITLCNRNRIKLPFIKKE GTGKAPKSRKSVLGLGP*VHT SPGDPAEGEGLPAGERPDGNLS QSPNSLRFYIKKKKAYK
12676	43044	A	12753	9	731	

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12677	43045	A	12754	143	641	RSWVLLGVGARGSTPRTYQVP SPSLAPSAALC*VS*VPLESLSCH ADNWKQELTKFISPDQLPVEFG GTMTDPDGNPKCLTKINYGGE VPKSYYLCKQVRLQYEHTRSV GRGSSLQVENEILFPGCGCLRVL RFYNTYSLVHSKRISYTVLELL PDQTFMEKMEKF
12678	43046	A	12755	1	1506	
12679	43047	A	12756	2	526	CQPVRAA*RHGNTPLATV*PAS T/WWWSEKQKEEQEMQNW ESAS/VSGYPDILSCAMSONPR KRRKPRNVSAPPVHQAQMNI SVEQMETSQTHQATPLTWGQM KRLAHVAEENLRSONKPLTTSN LMVAMMVVISLAVSLPVAGAD QNYIYWAIYIPFPF
12680	43048	A	12757	1	1443	
12681	43049	A	12758	3	766	
12682	43050	A	12759	29	253	
12683	43051	A	12760	34	252	
12684	43052	A	12761	1362	1611	SSVLHPWDARLVQHTKSIHH HINRTNDKNHMIISIDAFAFD KIQQDFMLKTLNKLIGDGTLYK IVRATYDKPTASILNG
12685	43053	B	12762	1	1755	
12686	43054	A	12763	1	2109	
12687	43055	B	12764	1	1497	
12688	43056	B	12765	1	1527	
12689	43057	B	12766	1	1746	
12690	43058	B	12767	1	2853	
12691	43059	B	12768	1	1479	
12692	43060	B	12769	1	1932	
12693	43061	A	12770	1269	1581	NTGKPNPAAHQKGYPPRSSGPH PWDARLVQHTKSIHHHINRT KDKNHMIISIDAFAFDKIQLPF MLKTLKSLGVSYNMFRTLTIPI AQVDTRGNQLPSYLI
12694	43062	B	12771	1	4404	
12695	43063	B	12772	56	2080	
12696	43064	B	12773	1	5445	
12697	43065	B	12774	295	2831	
12698	43066	A	12775	89	459	
12699	43067	A	12776	2	980	
12700	43068	A	12777	1	378	
12701	43069	A	12778	1	363	PGVALPGRRCRQAPADLLP*MR AYWPDVIYSFANRSRFBKHEW EKHGTCAAQV DALNSQNYFG TSLELYRELDLNSVLLKLGKPS INYYQVADFKDALARVYGVIP KIQCLPPSQDEDRQ

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12702	43070	A	12779	1	577	QRFKNDRCRDPRTGPIHGLWPD KSEG/CNRSW/PFNLEEIKDLCP EMRAYWPDVIHSFPNRSRFWK HEWEKHGTCAAQVDALNSQK KYFGRSLEYRELDL/NQVADF KDALARVYGVIPKIQCLPPSQD EEVQTIGQIEICLT.KQDQQLQN CTEPGEQSPKQEVWLANGAA ESRGLRVCEDGPVFYPPPKKTK
12703	43071	A	12780	1	624	MRPAALRGALLGCLCLALLCL GGADKRLRASVSRRPFSLEHPEP GHCLDLHLRAYPAR/WSS*PWP QDFWVR*PTWES/VSDLLPEMR AYWPDVIHSFPNRSRFWKHEW EKHGTCAAQVDALNSQKKYFG RSLEYRELDLNRGERVPTQFP RELVVNRSLAPPTPGFLSGHVI SVHTSSPLPSAMSGSFLRPLPEA ESGMLLGQPADP
12704	43072	A	12781	1	612	
12705	43073	A	12782	113	1149	RGAPRGPGRQGCCGHSRSPAR GPRDTGLGRPRAPGAPGGRCCS GGSAAGRLGDSVSPGLPRAA GGKWEPERQLAAFSQVGTMR PAALRGALLGCLCLALLCLGG ADKRLRDNHEWKKLIMVQHW PETVCEKIQNDCRDPDPYWTIH GLWPKDSEGCNRSW/PFNLEE KDILLPEMRAYWPDVIHSFPNRS RFWKHE/WPKRHGTCAAQVD ALNSQKKYFGRSLEYRKLDL NSVL/LKLGKPSINYQVADFK DALARVYGVIPKIQCLPTSQGE EVQTIGQ/IDLCLIKARTQLQN CTEPGEQSPKQEVWLANGAA AESRGLRVCEDGPVFYPPPKKT
12706	43074	A	12783	2	515	
12707	43075	B	12784	62	359	
12708	43076	B	12785	219	523	
12709	43077	A	12786	1010	1550	DTENIPSSRRRERSKVPYIVRQC VEEIERRGMEVGYHVSGR/V AADIQALKAAFNVSECRPAQD GMEVWAVVSAMRSQSA PRPRH VTSFSVSFLHLGSSRRPLHFRA LSNNKDVSVMMSEMDVNAIA GSLKLYFRELPFLTFDEFYPNF AEGIGEHWRPWP HGRRLLVH CCPQRL

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12710	43078	A	12787	2	951	GSNLYCTLEGDSFGYFVNKAK TRVYRD/THADPNWNEEFIEL EGSQT/LRLCYEKCYNKTKIPKE DGESTDRLMGKGQVQLDPQAL QDRDWQRTVIAMNGIEVKLSV KFNSREFSLKRMPSRKQTGVFG VKIAVVTKRERSKV/PYI/VRQC VEIEPPKALEGGWASTACPAG VATDIQALKAADFNNKDVSV MMSEMDVNAIAGTLNLYFREL PEPLFT\DEFYPNFAEG/IRVAEK EAVNNM/SLIINLATVFGPTLLR PSEKESKLPANPS/QPITMTDSW SLEVMQVQVLLYFLQLEAIPA PDSKRQSILFSTEV
12711	43079	A	12788	3	644	
12712	43080	A	12789	168	378	
12713	43081	A	12790	1	486	
12714	43082	A	12792	83	536	
12715	43083	A	12793	1	662	
12716	43084	A	12794	3	357	
12717	43085	A	12795	2	421	
12718	43086	A	12796	2	908	
12719	43087	A	12797	1	846	
12720	43088	C	12798	87	413	
12721	43089	A	12799	1	508	MCQGDYAWGGHMCRRGHLR RGHSHERDTPRGPERPPRPAR DRESKDERRRPPPKDPPAVRT\/ PDSPTATPPPPPPPPPPPPPPPP PAAPSAFAALRLRGPGRKWT RGQLPLPATAPPEARVRALPRGG YSSPGRATSARGAPWPLPSRT GKPPRPCSANTQEHC
12722	43090	A	12800	1	393	
12723	43091	A	12801	1	582	
12724	43092	A	12802	1	1422	
12725	43093	A	12803	1	1080	
12726	43094	A	12804	2	261	SCPFGGNCFYKHAYPDGREET QRQKVGTTSSRYAQRNRNHFWE LIEERENSNPFDNDEEEVVTLE GE/MLLMLLAAGGDDDELNTS
12727	43095	B	12805	60	802	
12728	43096	A	12806	2	238	
12729	43097	A	12807	1	1017	
12730	43098	B	12808	1	939	
12731	43099	A	12809	1	708	

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12732	43100	A	12810	1	2653	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDYRNHLP ESTEYTFSSAPHHYTSKIDHILG SKAPLSKYRRSEIKINCLSDHSA IKLELRIKKLTQNRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDDTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLARLIKRR EKNQIHAIKNDKGMSTNHTEI QTTIREYYKHLANKLENLKEI DKFLETYSPLNQEEVESLNR PITGSEIEAIIISLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSEL PFTIASKRMKYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNI PCSWVGRINIVKMAIL PKNWKKTTLKFIVNQKRARIA KSILSQKNKAGGIMLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEIMPHIYNHLIFDKPDK NKKWKGKDSL FNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK DLNVRPKTIKLTLEENPGNTIQDI GMGEDFMSKTPEAMATKAKID KWDLIKLSFCTAKETTIRLNR PPTEWEKIFAIYSSDKGLISRIYN ELQQIYEKKTNPNPIKKWAKDM NRHLSKEDIYAAKRHMKKCAS
12733	43101	B	12811	1	2748	
12734	43102	A	12812	1	1962	
12735	43103	B	12813	1	1833	
12736	43104	A	12814	176	421	QQPASPTRSVLLFPKTAHISGSP APPNVGLLNPSTGAQKKTMT SAGLGRLSL*K*LNLPCEVACA GETWVTSMMSGNQCN

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12737	43105	A	12815	1	1615	LISNFSKVSQYKINVKQSQAF L YTNNRQTESQIMSELPFTIASKR M KYLGIQPTRDMKDLFKENYK P LLNEIKEDTNKWKNI PCSWVG R INIVKMAILPKNWKKTTLKF I WNQKRARIAKSILSQKNKAGGI M LPDFKLYYKATITKTAWYWY Q NRDIQWNRTEPSEIMPHIYN H LIIDKPKDKKKWGDLSL FNK W CWENWLAICRKLKLDPLTP Y TKINSRWIKDLNVRPKTIKTL E ENPGNTIQDIGMGEDFMSKTPE A MATKAKIDKWDLIKLSFCT A KETTIRLNRPPTEWEKIFAIYS S DKGLISRIYNELQYIEKKTNN P IKKWAKDMNRHLSKEDIYAA K RHMKKCASSLAIREIQIKTTM R YHLTPVRMAIKKSGNNRCW R GCGEIGTLLHCWWDCCLVQP L WKS VWRFLRDLEIPFDPAP L LGIYPKDYKSCCYEDTCTHMF I VALFTIAKTWNQPKCPTMIDW I KKMWHIYTM EYYADIKKDEF M SFVRTRMKLETILSKISQIEK K TKHRMFSLIGGN
12738	43106	A	12816	1	996	
12739	43107	A	12817	1	756	
12740	43108	A	12818	1	1428	

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12741	43109	A	12819	1	2377	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NIVQHINRTNDKNHIIISDAEK AFDKIQQRFMLKTLNKLIGIDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTTRQGCPSPLLFNIV LEVLAIRAIQKEFIKGIQIRKFE IKLSLFADDMMIVHLENPIVSAQN LLKLIDNFSKVSQGYKINVOQSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGIGQLTRDVKDLFKEN YKPLLDNIKEDTNKWNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIVN QKGARIAKSILYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKGWNGDS LFNKWCWENWLAICRKLKLDLP FLIPYTKINSRWIKDLNVRPKTI KTLLENLNGTIQDIAMGKDFMS KTPKAMATKAKIDKWDNLNLK SFCTAKETTIRVNRQPIEWEIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSLAIREMHI KTTMRHHLTSVRMAIIKKLGN DWCWRGCGEIGRLLHCWWD KLVQPLWKSVMWFRFLRDELET PFDPATPALLGIYPKDYKSCCYK DICT/RVCVPAALFTIANTWNPT
12742	43110	A	12820	1	4840	
12743	43111	A	12821	578	630	EYKNR*GLSLNPWGKTVHISW DVWSVGSSKAKRNWESWES*C RGIQKASLSRSTGNHSASSGI* ESRV*GLGTTGYRGITASLSML RSCTRLH
12744	43112	A	12822	8	214	EEWPKRKSEIRERPRP*SWPSDK QTLVVQRGQKMEQANHPDPTD HMSQLMWTACPKGLGIALICL VRH
12745	43113	A	12823	33	240	GGGRTNLQAVPGFPGW*RTL RTAVWDRRLTLRKPHHCPGGS QFPGPQRQVIGLLHLFSSLNHQ GWFV

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12746	43114	A	12824	1	411	MSTITQRKEENPSVFLEWLWEA /CKKIYSPVTRLTRGSDPKR*V YYAISHRYQQKAPKPSGPG*TK SGGIIKPGNLGVLY*GPRGTGQ KGKARSEKGCSSLHGPGQTNKP WWFREDRKWSRPITWYGFSLV WFARTP
12747	43115	A	12825	1	611	
12748	43116	A	12826	120	493	KYRAQRRIARWLPQDLERGE AMLPNSSGWYKSLKGI/VLISEA FSCCKRAASLTADWL*VKQHS SPKKVQSPFSAVRRSKPWQFW RVTAAKQSIWDCRVRFIDVISC KLRLPLRVCGSRILK
12749	43117	A	12827	1	2195	VGEEGPAGVEGLNFFAQSRRLP GPQQCSPGAEGGASARARRPRP RPRPAAAMVPGVPGA/VLTCLW LAASSG/SWRPAPARL/CAAAG RVAVCRERPARS/CASRCLSLQI TRISAFFQHFNNGSLVWCQNH KQCSKCLEPCKESGDLRKHQ QSFCEPLFPKKS YECLTSCEFLK YILLVKQGDCAPEKASGFAAA CVESCEVDNECSGVKKCCSNG CGHTCQVPKTLVKGVPLKPRK ELRFTELQSGQLEVKWSSKFNI SIEPVIVVQQRWNYGIHPSED DATHWQTVAAQTTDERVQLTDI RPSRWYQFRVA/VNVHGTRGF TAPSKHFRSSKDPSPAPPANLR LANSTVNSDG/AV*TVTIVWDL PEEPDIPVHHYKVFWSWMVSS KSLVPTKKRKRRTDGFQNSVI LEKLQPDQDYYVELQAITYWG QTRLKSAKVS/LHFTSTHATNNK EQLVK/ITRKGIGITQLPFQRRRP TRPLEVGAPFYQDQQLQVKVY WKKTEDPTVNRVHVRWFPEAC AHNRITGSEASSGMTHENYIIL QDLSFCKYKVTVPQIRPKSHS KAEAVFTTTPCSALKGKSHKPI GCLGEAGHVLKSLVAKPENLS ASFIVQDVNITGHFSWKMAKA NLVQPMTGQVTVAEVTTESR QNSLPNSHSQSLPSDHYVLT PNLRPSTLYRLEVQVLTGEGG
12750	43118	A	12828	1	1410	
12751	43119	A	12829	2	299	
12752	43120	B	12830	81	510	
12753	43121	A	12831	3	436	
12754	43122	A	12832	1	769	

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12755	43123	A	12833	15	413	ERM CAGPWRKGAETGPYFCND TVRHRKASLLCPF*RMNGDQN SDVYAQEQDQFVQHFSQIVRVL TEDEMGHPEIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFRELE VEPRKQDADSLQRAWTVGWC VELLQA
12756	43124	A	12834	1	795	MNGDQKSDVYAQEQDQFFQH SQIVGVLTEDMGHSEIGDAIA RLKDVLEYNAGGKYHRGLTV LVAFQELDAINYAILLEACIYYL LKLYCQAQPYVNLIELFLQISC QPEIGQTLDLITAP/QDNVDFGR FT/EKQHANA*KILLEI/GEFFQI QDGYLDLFGDPTVTRKVGTDIQ DNKCSWL VVQCLQRSTLEQYQ ILKENYGGKKAKKV VQVKALY EELDLPVFLQY EEDGYSHIMG LTEQYAAPLLPAMFLGLVYKIY
12757	43125	B	12835	1	328	
12758	43126	A	12836	2	868	
12759	43127	B	12837	118	1138	
12760	43128	A	12838	100	374	KHISPALKALELPFRNLII/PLQ LLKVRILKEGEM/LDI*HWFL** GMGT VQKGMPHKCYHGKTGR VYNVTQHAVGIVVNNQVK*VV
12761	43129	A	12839	1	1035	
12762	43130	A	12840	13	600	INPPPPFRPELPSSNSPKMTDH KGERGEATRYMFSRPFKKTMG VVPLGHNN*RFYKKGDIVD/IK GMGYCVQNGMP/HKCYWPVKL EGVLQLLPQHA\VAIVVNQPV GQSFFPRE*IVRIEHIKHF*EPEIS FLK/RVLKENDSEKERSPNEKG TWGNSLKRILAPPQKKHTL*R TNGKEPELLEPIPEFHGHN
12763	43131	A	12841	1	317	QRPSEAKEIKLYAQIPPIEKMDA LSMLANCEKLSLSTNCIEKIAN LNLAEAVGDTLEELWISYNFIE KLKGIHIMKKLILYMSNNLVK DWGTPVIKGEDEEDN
12764	43132	A	12842	155	588	
12765	43133	A	12843	1	954	
12766	43134	A	12844	1	486	
12767	43135	A	12845	1	367	
12768	43136	A	12846	1	190	LISRAKEDMTLNI AEGVHPSY NIVLNTLHTCGISVKSTWRPSK GAAP*ARMPGGTAGPCLAS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12769	43137	A	12847	1	2376	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFNDRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLHQAQLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP C'WRA\WQQLPC*YKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
12770	43138	A	12848	1	636	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFNDRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLHQAQLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP C'WRA\WQQLPC*YKKQIS
12771	43139	B	12849	180	811	
12772	43140	A	12850	1008	1265	FLGVPTLGGWRPIQHRLK/PRE VTPVLLRDLIRRFPLWIGSDN GPAFLAALVQKTAQGIQNNITG GVYTLCDIDSHILFRSGY
12773	43141	B	12851	1	996	
12774	43142	A	12852	1251	1424	DSPRGEAES*A*LPEKLEMSG NRLVDNKDPGKKQTQRRIPHSP SQIPVPLPEIWCT
12775	43143	A	12853	1	1121	
12776	43144	A	12854	189	621	
12777	43145	A	12855	2207	2308	
12778	43146	A	12856	1	762	
12779	43147	A	12857	1	678	
12780	43148	A	12858	3	496	
12781	43149	A	12859	107	258	NALGKRSTFTNRNFLASGRFLD SVTYARRLQYQYAPL*KTAI*SF SLLNH
12782	43150	A	12860	2	410	SPDPVWSTYKSTCHIAQEAKEI HLRNQYERKGE*APRSLNMSE DANGGAPNPWFEEPEETIGW GFDEIRQQQHNIIR*QDAGLDA LSSHSRQKQM/GIEIGNELHEQN EIHDDLANLMENTDEKLRNETR RVN
12783	43151	A	12861	3	1402	

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12784	43152	A	12862	1	711	MAPDPWFSTYDSTCQIAQIEAE KIQRNQYERKGEKAPKLVTVI RALLQNLKEKIALLLKDLLRAV STHQITQLEGDRRQNLDDLVT RERLLASFKNEGAEPDLIRSSL MSEEA KRGA PN PWLFEEPEETR GLGFDFIRQQPKINQEQDARL DALSSIISSQKQ/MGQIEGNELD EQNEIIDDLANLVENTDEKLRN ETRRVNMVDRKSASCGMIMVI LLL.LVAIVVVAVWPTN
12785	43153	A	12863	1	936	
12786	43154	A	12864	1	1023	
12787	43155	A	12865	1606	2238	
12788	43156	A	12866	3	347	
12789	43157	A	12867	1	1665	
12790	43158	A	12868	1	589	
12791	43159	A	12869	19	1677	
12792	43160	A	12870	1	906	
12793	43161	A	12871	1	228	
12794	43162	A	12872	1	320	
12795	43163	A	12873	1	398	TSKAPGAQGEQGFEECLAVALL AGRPPLSLWALFQATTPVLQ LKEAFFRPEVPLRRDLPLLLFR TQTSDPAMLPTMIGLLAEARR AGCLSYQTSLSVDGETWHVMG ISSLLPSLEGWKQHVTEAFQF HF
12796	43164	A	12874	3	322	SAGGSGRRTLHSRTMAQFVRN LVEKTPALVNAAVTYSKPLRAT FWYYAKVELVPPTPAEIPRAIQS LKKIVNSAQTSFKQLTVKVTT G*MKT DVHNRKCLPLGFF
12797	43165	A	12875	91	425	WTFHPTTMAPFVRDLGEKTPA LGKAAVTVLKPRLAAFWYYH QVELVPPTPAEIPRAIQSLKKIV NSAQTSFKQLTVKEAILLNDL VATEVSTWFYVREITGKRGIIG* NV
12798	43166	A	12876	179	664	HSSPAVPGRTDFSHSQNPWPQF CPVTLVGEDPRALVNAAVT/YT RKPRIGLHFYYAAKVELVPPT PAEIPRAIQSLKKIVNSAQTTG LANSSHVKEA/VL*NLVATEVA LMWFLCSERLLGKRGHSLGYG CFEDQSFNIIWFILFILELVFW DHVDPDC
12799	43167	A	12877	25	164	
12800	43168	A	12878	2110	2260	
12801	43169	C	12879	32	1429	
12802	43170	A	12880	172	322	

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12803	43171	A	12881	1060	12039	
12804	43172	A	12882	1	810	
12805	43173	A	12883	3	146	
12806	43174	A	12884	1	1211	GPQDGNQQAPPEKVGWVRKF CGKGIFREIWKNRYVVLKGDQ LYISEKEVKDEKNIQEVFDLSD YEKCEELRKSKSRSKNHKFT LAHKKQPGNTAPNLIFLAVSPEE KESWINALNSAITRAKNRILDE VTVEEDSYLAHPTDRRAKIQHS RRPPTRGHLMVAVSTSTSDGM LTLDLIQEEDPSPPEPTSCAESFR VDLDKSAVQLAGSRRRADSDRI QPSADRASSLSRPWEKTDKGAT YTPQAPKKLTPTEKGRCASLEEI LSQRYAASAHTLQLRAEEPPTP ALPNPGQLSRIQDLVARKLEET QELLAEVQGLGDGKRKAKDPP S/RSPDPSES/EQLL\ETER/LLG EASSNWSQAKRVLQVRELRLD LYRQ/MDLQTPD/SHL/RQTTPH SQ/YRKSLM
12807	43175	A	12885	617	1041	TTLINPGGPAPLLSLPTSSITGFT TFYHPNLKPLRTCPSPVQAWPC RHPPI*SRDYQRDAEPTTCISKLL GENIRRDDEFWKVQIKARSGETE QNPRSTAFAGELPLANREELN LLLNKGILPLCDQRQEIESECAF TIFCAGDANCFFPSPHTLPLTAL QQRPCGLSGSASKEAWGNSLV CGPRGDTLPMAIAKPHRSASKH STLHQYPTPPRSLCHQHRDEQP TNHLQTLNTIPA WHTKWVPL DHINKPWRS CSSQSAYLFYHW LHYFLPPKLKTSKDL SILSAGLA MSAPHILFRVSAITNSNCKPSS TSKACEELFKHQCLGSTDPIH IQGGAPFSAVSPQRLVLRGSQD GSHMVRPRLPPFDSAGLANFHL FSKFLD
12808	43176	A	12886	1	606	
12809	43177	A	12887	174	350	VSWRFVQVFI*VAGGSRICAAA GLSPGTPPCATSLIGACSLIFIP RLLSLFCGDEAL
12810	43178	A	12888	3	265	
12811	43179	A	12889	1	1209	
12812	43180	A	12890	53	369	VAHQEKGIAEPLRPTGDSRQT HRRLDVERSTSVQEHMGGCHF SPFPEREKLSTLRGIHQAPAL WQATDQWIDIEF/GLGQPEESL GR*ITRLQGGKTLFPFGSPIC

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12813	43181	A	12891	1	345	
12814	43182	A	12892	2	451	
12815	43183	A	12893	2	286	
12816	43184	A	12894	217	1071	GENPRSENTRLATILEVACCHF GSSPPPSIGSSGRKDPPLTFGDH EGTSKAEPSPALGLTPEHKGNV GHAARIQQPGPLSLWSRKAGK GVQDCYIDLKQIKIDLDKFSND PDGYIDVLQGLGQSFDTWRNI MLLLNQTLTPNERSATTTAARE FGDLWYLSQVNDRIAAEKREK FLTGGQAVPSVSGSIHWDTESEH GDWCCRHLITCMLEGLRKRTRK KPMNYSMMSTITQKKEENPTA FLERLREALRKHTSLSDSIEGQ LILKDTFITQSAADIRK\NFKSPP
12817	43185	A	12895	1	756	
12818	43186	A	12896	473	1015	
12819	43187	C	12897	152	322	
12820	43188	A	12898	146	1079	PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAPWKIPFLGIREAKN PRSENTRLATILEAGHRHLGTS VSKDHPVTFWRPRRDLQSDLK QIKIDLKGFSDNPDGYIDVLQEL GQSFDTLWRDIMLLNQTLTPN ERSATITAAREFGDLWYISQVV AAVAGLVSEAVKIIQGSYCVDI HDVNGILTAKGDLWLSDNHLL KYQALLLEGVPLRLRATCATLNP ATFLPDNEEKIEHNCCQVIAQT
12821	43189	A	12899	189	1798	

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12822	43190	A	12900	194	1729	NPAAQTFFVVKKGGRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSSPCNTPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEAEWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVL PQGFRDSLH LFGQALAQDLSQFSYLDLTVLQ YMDDLLLVTHSETWCHQATQA LLNFLATCGYKVSQKNAQLCS QQVKNLGLKLSKGTRALSEERI QPILAYPHPKTLKQLRGFLGITS FCRIWIPRIKAVKLQILQMEPQ MQSMTKIYHGPLDRPTSPSSNV NDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAAP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPIN*SMISTI TQKKEENPTAFLERLREALRKH
12823	43191	A	12901	1	642	
12824	43192	C	12902	54	254	
12825	43193	A	12903	32	221	NGVGHNRMTNGSGGGGEWGP PAPASA*GCSLASAFASAPRW WFEMGCRGIYDAQVALSRSF
12826	43194	A	12904	203	538	
12827	43195	B	12905	131	536	
12828	43196	A	12906	1	1251	
12829	43197	A	12907	38	475	ESERRGEFCLCKIIESEGRAVCV EDEQTSHFALTGNNGIYRKSQQ QWQQLSDLARDPPAQCSAGP VGDDMFHWQATIMGPNDSPYQ GGVFLLTIHPTDYPFKPPKVA VTTIRIYHPNINSNGSICLDILRSQ WSPAFNQFPKSS
12830	43198	A	12908	282	849	QSCPAAGIISFGRTFEHTPREV RKPDCKHTLLALKRINKDLSDL ARDPPAQCSAGPVGDDMFHW QATIMGPNDSPYQGGVFLLTIH FPTNDYPFKPP*GLHFTTRFYHP ININSKWAACFLRYS*DSQWSP ALTFKVLLSICLLCDPNPD DPLVPGDWHGYS*NRGTGDKYN RISREWTQKYAM
12831	43199	A	12909	1	397	
12832	43200	A	12910	245	535	
12833	43201	B	12911	68	333	
12834	43202	A	12912	265	562	

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12835	43203	A	12913	1	872	MVNTCEQLDWIEGCKVLILGVS KEASQGLGGRSRGRNVQRSTD ADIRPTSEKDARSLMTTRQEDN ISVDQRGFLSGVQKKGSCANGL KGSVCGGFYVWMAVIRMGVG KAMGLNLKLGKFEIKKGYLKG CRDSLRLSPTGFGKFTATSHV AATVPKVVLELTLQTHKILRG VFAHLTSLQLHSLPPGSSMDS AKARRQLQVAGQGHSLVKQK GFHVEAPDHHVPQLSDISCKSY RWGHKLIKINFLIPPLWYYDL EEVKREQSEKQQAAMADIIIG DALNAQKAFKGNPKGHKPLPF SAGQMENW*CCECPKSI
12836	43204	A	12914	7	231	
12837	43205	A	12915	1	223	MEILITCDKGLIFTGNTRKSETS TSECTCPDLINCSLSHSPSPSDE ETQHHTDLSLHVRPRKGYLLCIY HIPDIVAVMVNIQCQLDWIEGC KVLFLGVSVKVLPEINTGISGL GKADPPSIWKS*QHVTKDLYLQ VILENQKLVANALVRWLTVP FPTLLRALQMRKHSTTLTVCMS DRGKDICYCASTIYQI
12838	43206	A	12916	1083	1273	NKMSFKLKEDCFGRSKCNLT* CWKSINEA*/K/DLELQLQFGPQE KLFALEQQVKKKLNLPDA
12839	43207	C	12917	1	1506	
12840	43208	A	12918	3	1219	
12841	43209	A	12919	1	735	
12842	43210	A	12920	2	94	
12843	43211	A	12921	362	460	WLILSVNLIGLKDAKYCSCVCL *GCCQRRLTF
12844	43212	A	12922	1235	1474	
12845	43213	A	12923	1	250	
12846	43214	A	12924	1	261	
12847	43215	A	12925	2	85	
12848	43216	A	12926	1	291	
12849	43217	A	12927	1	321	
12850	43218	A	12928	1	370	
12851	43219	A	12929	1	684	
12852	43220	C	12930	1	210	
12853	43221	A	12931	2	91	
12854	43222	A	12932	1	243	
12855	43223	A	12933	2	353	WMKLETHLSKLS*GQKTKHRM SSLIGSTDQQLRVVKNVQGRVC PGSTGHGAWEAWTAMRKVDS PLQTGSLRPGWCRQVGSNARS GSAEAGNPGIHPGICPRVEDG IQAENFFEV

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12856	43224	C	12934	1	289	
12857	43225	A	12935	1	1194	
12858	43226	A	12936	140	237	
12859	43227	A	12937	1	292	
12860	43228	A	12938	2	178	
12861	43229	B	12939	1	1245	
12862	43230	A	12940	2	241	
12863	43231	A	12941	1	675	
12864	43232	A	12942	1515	1920	TPTNLQEKKNKQPHQKVGEGYE QTLKRRRLCSQKTHGKNAHH HWPSEKCKSKPQWIPSIHQLE WQSLKSEQTTGTWMLKLETHLS KLLQGQKTKHHMFSLIGGNRT RRTHGHRKGNITLWGLSDSV NCASSG
12865	43233	A	12943	608	891	
12866	43234	A	12944	1	3956	MGSCPGGFTAIFYQRYKEELVP FLLLKLFQSEKQGTLPNSFYEAS IILIPKPRDRTTKENFRPISLMN IDAKILNKILTNRIQQHIKLLIHH DQVGFHGMQGWFNIRKSNVI QHINRTNDKKHMIISDAEKAF DKIQPFMLKTLNKLGTWMLK ETIILSKRSQGQKTKHRMFSLV NIIPITIKILKQNMATMETLCPIF KLEGDTMDNPIANRRVRTAVP TSVVCLHVGTEPEARLPHGPMI TAQSPFG
12867	43235	A	12945	1	855	
12868	43236	A	12946	1	255	
12869	43237	A	12947	273	3484	
12870	43238	A	12948	3	377	
12871	43239	A	12949	85	333	
12872	43240	A	12952	22	308	
12873	43241	B	12953	30	383	
12874	43242	A	12954	3	448	
12875	43243	A	12955	1	453	
12876	43244	A	12956	3	491	
12877	43245	A	12957	2	749	
12878	43246	A	12958	155	637	
12879	43247	A	12959	1	510	
12880	43248	A	12960	2	559	RPHASAHASGRQSQDVTTMV WALLLLTLTLTQGTGSAQSAL TQPPSASGSPGQSITISCTGLIND VASYNFVSWYQQHPGKAPKL MIYEVTKRPSGVPDRFSGSKSG INTASLDHLWGSRLDEADYYC LLICRRLHPGGIRRDWPRVTV LGSAQRPTPTVTSGSRPSSEGAP SQQGHTSVSDQ

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12881	43249	A	12961	1	1958	MSVQRKDRVRTQQGGSVASSM LTQEPVGSVALGQSARDRDPD CSDSVSVYLMDTWQSVIIGFAE SAATLGDPPELPMHPEGSEASY ELTQPPSVSVSPQQTARITCSGD ALPKQYAYWYQQKPGQAPVL VIYKDSERPSGIPERFSGSSGTT VTLTISGVQAEDEADYYCQSAD SSGTYPTVTQADRETPTHQYSR HPSYAKGFVFLWGSWAQSALT QPASVSGSPGQSITISCTGTSSD VGSYNLWSWYQQPQKAPKL MIYE/VDSKRPSGVSNRFGSKS GNTASLTISGVPGLRDEGDDY CCSYAGSVASYELTQLPSVSVS PGQTARITCSGDVLGENYADW YQQKPGQAPELVIYEDSERYPG IPERFSGTSGNTTTLTISRVLTE DEADYYCLSGDEDNPSVTQAD GEDTGIRSHYEGTLALYLYPEP VKATCSVTSYVLTPPPSVSVAP GQTARITCGGNNIGSKSVHWY QQKPGQAPVLVYDDSDRPSGI PERFSGSNSGNTATLTISRVEAG DEADYYCQSLSTLGPCTLGDTV LRPMIYSVSIQASGVDPGFSGSK SGNTASMTISGFQAEDEADYYC NSHRRGSVVSSELTDPAVSVA LGQTVRITCQGDLSRYYASW YQQHPGKAPKLIYDGH
12882	43250	A	12962	2	367	
12883	43251	A	12963	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12884	43252	A	12964	2	1178	
12885	43253	A	12965	1	732	
12886	43254	B	12966	99	716	
12887	43255	A	12967	1	1011	

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12888	43256	A	12968	3	1263	GRTIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERSAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTQRYSS RRATPRHIVRFTKVEMKEKMG LLVPNWTNHSPLFRALFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSPGEGGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQERQRTQRY YSSRRATPRHIVRFTKVEMKE KMLRAAREKGRVTLKKGPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTTPALKELL KEALNMERNNRYQPLQNHAK
12889	43257	A	12969	1	1392	
12890	43258	A	12970	1	1224	
12891	43259	A	12971	1	970	
12892	43260	A	12972	1	954	MDGDLHKGVAVFWPPDAAGG HTCCRSMVCRSLGGAQWKFH SFRCRIRFELIHHMIQERNISIN QKDVHTETPSETHHHQRPKVD KSMKMRRNQCKKAENSKNQK ASSPPEKHNWSRAREQNWTE EFDKLTVEGFRRWVITNSSELK EHILTQCKEAKNLEKTLEELLT RITSLEKNINDLMKLKNTA*EL REAYTSINSQISQAERISEIEDQ LNEMKHEHRIREKRMKRNKQS FQEIWDYVKRPNLRLISVPESD GENGNK*ENILQDIIQENFPNL ARQANIQIQERQRTQRYSSRRA TPRHIVRFTKV
12893	43261	B	12973	1	1346	
12894	43262	A	12974	1	318	GSRGELLSLCYNPSANSIIVNII KARNLKAMDIGGTSDPYVKVW LMYKDKRVEKKKTVTMKRNL NPNFNES'FAFDIP\TEK\LRRETTII ITVMDKDKLSRNDVIGK
12895	43263	A	12975	17	389	SWGPHCTHKLKSFSLMPMT DAMDREMR/RGSKKDVR/*VLG GCAATWTPRAGGRQQSPGTTV DKREDTPDCAMDQSTSHIPISA SSPSLLPGSSFTQTFFPGIAHYR ASFLIVAYYPSNKNKSK

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12896	43264	A	12976	84	282	GEGQVGWVPQGEVQQDEEVIEE VGA* DAGSGYQEEEEGPQLRR EVVGVELVVGADPSGEGPKED
12897	43265	A	12977	1	1179	
12898	43266	A	12978	3	634	
12899	43267	A	12979	234	619	CYVVQEVLPDLLCHLVICSRP GRTAEWPPG*GF*SPPHRGW/ GC*GHD/HRRGTSIFPTH/V*SPP ASYPGSLCRPGGQEEEREREGEW QREGRRPGTR*CGAAEARGW RAAAKATAVAGARRRRPGISG
12900	43268	A	12980	1	1182	
12901	43269	A	12981	3	763	
12902	43270	A	12982	32	949	
12903	43271	A	12983	1	1299	
12904	43272	A	12984	1	1176	
12905	43273	A	12985	1	421	
12906	43274	A	12986	81	404	VKFGPEIWCRRSDQGRGGVGT SLGRSIPCPALCSVRKIYLRPL VLRPTSPRNPILNRDPTVQLT WQPLPEPLELWPKAL*LTSPQIY SA*RLKTDAAARLPKPPR
12907	43275	A	12987	1	378	
12908	43276	C	12988	1	751	
12909	43277	A	12989	302	629	ICLSYPAPPKCRFPHYTRVLYH* SLFNENTSQSCFTSR/WKLESFT TRAIERHQIFLL*ATLTLIRWLD KKLAFQLLSLTASFSPSYQLSP TPPLKLPIISSHTRQMV
12910	43278	A	12990	14	380	
12911	43279	A	12991	189	608	QSDLSASQHGFLPLATEVRSSG AASCPDSDSICPAPTAPGRATP PQANCWASEGLTRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLSNLQGP RSRPVAFLSKQLDLTVLWGPSC LVVQQLPP
12912	43280	A	12992	1	513	
12913	43281	A	12993	2	462	WSMGLPRRSGCVSLQPLSQEDL GRSQSESLGPEFQGLWEWLPEQ LPRSFQALGSLSYFPRTLNLNLS WPLCLRKWGYL/SLYLPFQVGL PSTVPWPLILPSKVPEEEGQLQS TLPCGIKLLPVFTSHHAFGLGVFC NQWVSDVFLALFLMKLLGAQ
12914	43282	A	12994	59	213	
12915	43283	A	12995	1	1159	
12916	43284	C	12996	1	864	
12917	43285	A	12997	1	1155	

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12918	43286	A	12998	879	1163	SRRPLFMGLVRVLCCKMSGRGP LCFPGGHWIVFLWGGTVLWLW T*SPHWHRRKAN*DLFLQKLPRL *VSHQCDPCLPVCHLWNCLFL PLWGPPAG
12919	43287	A	12999	1	179	
12920	43288	C	13000	1	410	
12921	43289	A	13001	42	365	FGLRLSLAPPFCMFPLTT*HS*P SVLPASFPAAALGIPQARAVTFV SP*LLASLSFWAPPCSLCLDASV *HGSHLWHAQSSCRLRWSFGL AASQMQPPEPSHGPRRK
12922	43290	B	13002	1	741	
12923	43291	A	13003	8	265	
12924	43292	B	13004	1	646	
12925	43293	A	13005	1	1158	MKLVTIFLLVTISLCSYSGYWFE NEQMSVGGGDDNGEVLYSALR GASEVIGQCQSSATKPRRSKGE SVREPWARVPGALGVGVREID QTLGIDTILCHHERLLQSHYGI HKSSLSMVGNSQVAALYQLNV YVVADTVGLIKNSISLDSVQPN YCSNKHIELRTQVGGARNLRA NSPMTSSYNQESSSMENVVALS LLTVESPTSMFDYCDDSLERSVK SALDIFSMIIYTVTFFLAGNG LVIWVVGFMHSCVTNTCLPSPDP HLHGPLTCDPVANLVLEQLHTS KGNsgaledLAFGNLFLCSLLD LQGNsWWKvSPSLYNQYDLQ NETQGSQHLWKEIHPW*PSAFV V/SSGYWPENEQMSVGGGDDN GEV/RVFRPEGGFRGDRAVSFV SH*AEKIWEGISQRAL/VPEFQG LWEVW/CREIDQTLGIDTILCHH HERLLQSHYGIHKSSLSMVGNS QVAALYQLNVYVVADTVGLII KNSISLDSVQPNYCSNKHIELRT QVGGARNLRANSPTMTSSYNQE SSSMENVVALSLLTVESPTSMF DYCDDSLERSVKALDIFSMIIYT VTFFLAGNGLVIWVVGFMH SCTVNTCLPSPDPLHGPLTCDP VANLVLEQLHTSKGNsgaled LAFGNLFLCSLLDQGNsWWK VSPSLYNQYDLQNETQGSQHL WKEIHPWHQTLVTTAHFFFGFF

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12926	43294	A	13006	3	371	AGARFNVRSR*RNDRVRPHRD VYSLQGRSLSDHSPTFGCQQTQ GRLPWSFTLSGKFRFSGEGATT SPAHIKNFQTPEPQWP GIPPEPPP TGACYTCRKS GHWAKECPQAR IPPKPHPICVGP
12927	43295	A	13007	77	332	RWKKNCNLSPPRMS*QR*WKP* MQQAACSVGETQPPCTQVK*T ALLLTQSLFGGLFTRTHMKFGA VTRIGGPPLDQSPVLLLFAP
12928	43296	A	13008	1048	1349	RVVEQDDAERLFRFRFAA/GDL PYGAFGEIF*ETQCEMQQLAE DHASVTMISLEAWRLYRKMVC RIWASMLRLSVCHLCAPKR VV SLISRNGYHLP GSIH
12929	43297	A	13009	213	499	PEQRTSHRQQRQPPQSRSP FCPLSPRSALSLFLCDGYAAP* AYRE*IPVTEDHFAE*/ISWCP *YREALGQLLAKMRR*SARKRF QLSP
12930	43298	A	13010	2	431	
12931	43299	A	13011	2	367	
12932	43300	B	13012	1107	2083	
12933	43301	B	13013	1	627	
12934	43302	A	13014	712	2671	AHVGRGST*ALPRAMGSDAF*C PLQ*MTPASFGSKAALS RVFIKE ALMMEDPCVVRKPLSAHMTA WWCRIWKAYLESV
12935	43303	A	13015	50	1362	WEQIPHGLVLSLQQLPRRSGSIS LQPLSQEDLGRSQSESLGPEFQ GLWQWLSDFQT*HQWVVS GFQ AFSDRLKAALSASLLRFGDSD WLPSSSACKCLMLGLHFVIVGN ICATLKEKYSSMLHLDVTMKK NGEKRTLQKRKKGMPPHPAY EDLNIAAITLPANVVLHQPSGFR TSGQLDPVWWSLDTDAHEIWC QDPGLGSGDFPWEITPLSSYSLL HEKDPPTTSGPQTDQPKKHLTN FKSKTKETGFIHGPKTPAPVTD WEGSLPLVFNHCRDTS LIIHPCF KGVRRRDACLGPSPLAASPAF LEKGQDLINLAFKVYNNRKKL QFLASTVRQTPATSPA HKNFQT TEPQQPGVPPPEPPTGACYMCR KIWPLGQANARSPGFLSRVPS VWDPTGNRTVQLTWQPLPEPL ELWPKALCLTDSFPDLLGLAA
12936	43304	A	13016	1	507	
12937	43305	A	13017	5	271	
12938	43306	A	13018	1	618	

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12939	43307	A	13019	1	429	
12940	43308	A	13020	1	3567	
12941	43309	A	13021	1	353	
12942	43310	A	13022	1	338	
12943	43311	A	13023	1	1175	
12944	43312	A	13024	3	326	
12945	43313	A	13025	150	494	PSPSLGYLVGTRGTALRL*DAR AAMRPFDPSTLLPTCWDYWTY AGSLTTPLTESVTWIIQKEPVE VAPSQLSAFRTLLFSALGEEK MMVNNYRFLQPLMNRKVWAS FQATNEG
12946	43314	A	13026	2	975	DSREHHPLQTGVSGNRPKMLG RNTWTKTSAFSFLVEQMWAPLW SRSMRPFGRWCSQRSCAQWTSN NTLHPLWTVPVSPVGGTRQSPI NIQWRDSVYDPQLKPLRVSYE AASCLYIWNTRYLQVEFDDA TEASGISGGPLENHYRLKQFHF HWGAVNEGGEHTVDGHAYP AELHLVHWNWSVKYQNYKEAV VGENG LA VIGVFLKLAGHQT LQRLVDILPEIKHK\DARAAMR PFPDPSTLLPTCWDYWTYAGSLT TPLTESVTWIIQKEPVEVAPSQ LSAFRTLLFSALGEEKMMVN NYRFLQPLMNRKVWASFQATN
12947	43315	A	13027	1	1233	
12948	43316	A	13028	761	1000	IPFISFSLIALARTSNTMLNKG ERGHPSLVVPFIGNASSFCPVSM ILAVGLS*IALIILRYVPSIPNLLR VFSMKGC
12949	43317	B	13029	697	1527	
12950	43318	A	13030	1	1695	
12951	43319	A	13031	434	925	VAKIFSHFVCCFLTLMVVFAV QKLFSLIRSHLSILSFVAIDFGVL DMKSLPMPMS*MYMPRFSSRV FIVLGLTFKSLIHLELIFV*GVRK GSSFSFLHMASQFSQHLLNRE SFPHCLFFSGFSKIR*L*ICGIIE GSVMFH*SI SLFWYQYHVLVT VAL
12952	43320	A	13032	1124	1234	KITPKKQIRQSPNLTQNTGQQ*S LQLWEHFQISTHF
12953	43321	A	13033	929	1261	
12954	43322	A	13034	1118	1354	IPFISSCLIALARTSNTMLNRSGE RGHPCLVPVFKGNASSFPFSMI LAVGLS*IALIILRYIPSIPSLLRV FSVKGC

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12955	43323	A	13035	2	348	HQHLLFPDFLMIALTGMRWYL IVVLCISLRASDDEHF/YHVS GCINVFV*EISVHILRPLFDGVV* FFLVNLFKFFVDSGYEPFVRWV DCKNVLPFCRLPVIHSDGSFFCC AFAAL
12956	43324	A	13036	578	712	LISNFSKVSQYKINVPKSAFLY TKNRQTAKS*VNSHSQLQRE
12957	43325	A	13037	1	1833	
12958	43326	B	13038	1	1587	
12959	43327	B	13039	1	1851	
12960	43328	A	13040	1349	1444	
12961	43329	A	13041	953	1277	MVLPRESSRVFVVLGLTFKPLI HLELIFV*GVNFV*GSSFSFPHM ASQFSQHLLNRESFPFLFLSG LSKIR*L*MCGHISEGSLFHW ESLFWYQYHVLVTVAL
12962	43330	B	13042	804	4236	
12963	43331	A	13043	1	744	
12964	43332	A	13044	137	797	
12965	43333	A	13045	210	418	
12966	43334	A	13046	1	927	
12967	43335	A	13047	1	1415	MGFLGTGTWILVLPQAQPK PGGSQDKSLHNRELSAERPLNE QIAEAEEDKIKKTYPPENKPGQ SNYSFVDNLNLLRAITEKEKIEK ERQSIRSSPLDNKLNVEDVDST KNRKLIDDYDSTKSGLDHKKFQ DDPDGLHQLDGTPLTAEDIVHK IAARIYEENDRAVFDKIVSKLLN LGLITESQAHTLEDEVAEVLQK LISKEANNYEEDPNKPTSWTEN QAGKIPEKVTMPMAIQDGLAK GENDETVSNTLTLTNGLERRTK TYSEDNFRDFQYFPNFYALLKSI DSEKEAKEKETLITIMKTLIDFV KMMVKYGTISPEEGVSYLEGL DEMIALQTKNLEKINATDNIS KLFPAPSEKSHEETDSTKEEA KMEKEYGSLKDSTKDDSNPG GKTDEPKGKNRSPWPKIRKNI EWLKKHDKKGNKEDYDPFQR* EVSPNNKADAIYVEKGILDK AEAIRIYSSL
12968	43336	A	13048	1	879	
12969	43337	A	13049	3	640	
12970	43338	A	13050	134	382	DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPPWMN/WPPH*IKHIQS
12971	43339	A	13051	87	500	

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12972	43340	A	13052	1	1356	
12973	43341	A	13053	1	447	
12974	43342	A	13054	3	107	
12975	43343	A	13055	3	2377	
12976	43344	A	13056	1	2193	
12977	43345	A	13057	1	2724	
12978	43346	A	13058	253	490	QSSIPAIMSSFLGTGAETMPVPL GAGMRRTSTEPQVCFCTGIIF KTSSLREAPRKKSMSISLMGR E/WMPVTKLGRLLVKDMKIKSLE EIYLFSLPIKESIIIDFFLGASLKD EVLKIMPVQKQTRCGSVLVRLL PAPRGTGIVSAPVPKLLMMA GIDDCYTSARGCTATLGNF/AK ATFDAISKTYSYLTPDLWKETV FTKSPYQEFTHLVKTHTRVSV QRTQAPAVATT
12979	43347	A	13059	1	819	
12980	43348	A	13060	1	623	MARRKNGKWESEIDFCLGGSL KDEVLMKIMPVQKQTRAGQCTR FKAFVAIGDYNHGHLGIKCSK E/LATAIRRAILLAKLSIVPCRG YWGNKISKPHIVPCRGTGIVSA PVSKLLMMASINDCYTSARG CTAILGNFDKATFDAISKTYSYL TPNLWKETVFTKSPYQEFTHLV VKTYTRVSMQSTQAPALAKLP RVAVQPRAEV
12981	43349	A	13061	1	949	KWRITPVPTGRP/GGPGGPGMG KPRCF/RGEVFGIVIRAGSPGPG TGPGRG/GEAAGAKAED*E/WMP VTKLGRLLVKDMKIKSLEEIYLF FSLAIKKSEIMSFLGLLGRDE VFE*LCPVQEQ/TRAGQ/RATRF KAFVALTTLGTTNG/HVGLGC* VPPREVATGNSWGPFLGQALH SSPVRRLGLLGGTKNSAKPPTLV PWQR*PRAACGLCAGYAFIPLQ PRGQLASVSA/PVP/KKLLMMA GTDG/CNNSQRRGCTATVG/NL AKATTFDAISKTYSYLTPDLWK ETVFTKSPYQEFTHLVKTHTR VSVQRTQAPAGATT
12982	43350	A	13062	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIDACGQLE

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12983	43351	A	13063	2	797	NRVLLAMVNPVTFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIGLFAKVPKTAENFR/A L*SIEEKGFGL*GVPCFHRLFP VLCVRGGDFHTAINGTGGKSI\ YGEK\FEDENFILKHTGPGILSH GKMLDPNTNGSQFFICTAKTIE WLDGKHV\VFVKVKEGMNIVE AMEA\FGSRDCKTSKKITIA\DF GQLRIKFDFVFLSLTTKIISFCAL LSGEHPLHPIWLGVILESMWLS LAVPFVVPCFCSLPCLAGLQS
12984	43352	A	13064	1	720	
12985	43353	B	13065	98	2074	
12986	43354	A	13066	596	841	
12987	43355	A	13067	66	326	
12988	43356	A	13068	1	441	
12989	43357	A	13069	2	325	WCPSQAAAAGARATRDMPEGS MTCLCRALWWLFSWLKVHR*R QQQQGRPAAPSAGPAKPTPTRN SSWLLAAPVPTRTSPSTPPCKL REPAPALASPERGSHSAAVG
12990	43358	A	13070	38	1066	
12991	43359	B	13071	1	324	
12992	43360	A	13072	2	680	
12993	43361	A	13073	2	165	
12994	43362	A	13074	1	1110	MASLLKSARPTQHWKEETPETS KRLKEQTPDIPSLRAVTLIAKVH SFIPEVCETKNPLEGIHSGHILAP NVGSPSPRRQARVQVFENVSVR ATKSDLPQSSLWSRRKTTVSAA ASKKTSKEISKGPQKPPGY/PVT SPSSCRGRGIWPNP/EYMTSPS LI*/SQIKVDLGKISDDPDRYIDV LQGLGQTLDSLWRDVMLLLDQ TLAFNEKNAALAAAEQFGDTW YLSEVNDRMTAEERDKFPTED GEPIKDCDQIIVQTYAAQDDIL EVPLANPDNLNLYTDGSSFVENG IRRAGYAIIVSDVTILERPNLFRA IQQVVKACEVCQRKNPLVHPP NYLYKTLNLTHSLNLQSNPSLA NDCWLCSSLSVSAEPYN

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12995	43363	A	13075	450	1776	RGGRACLRP*AA/SPGPSTP*WP PPRGVQAAAILSGPPRPAPPKG AASQRLCGGFVEARQAWVGRR GRRGPVGETQPPPSVIQPPSRG AG/PRDQQPAMPEPTPSVGSC AARASQISAAPCSTAPSPIDHPR AEECRRTVWDWQAAPPAQV RDPLGEASWAPESGGDVENLY VLLRDCKYTSQHPVSSSGSVNA PIDTLYLATLLRDCKYTNRHVS SSSRFVNTPISTVSSEFANAPID TLHLATLKEETPNTSEHQKEQT PDMPLRTVTVTARVRGFILDV SETKNPPIPDITWRPWRDLRQS PSNQTLAFNEKNAALAAQEF GDTWYLSQVNDRMTAERDKF PTEFIPSSGFLVLLTSRMKPQTF AASVTALKDGVSRVCSFRCVQS FFLPSADWCYKPLARYALIG AFLQSAHWCVYKPLARHSVL GAFTNL
12996	43364	B	13076	1	1999	
12997	43365	A	13077	3	469	
12998	43366	A	13078	224	410	
12999	43367	A	13079	478	675	
13000	43368	C	13080	55	237	
13001	43369	A	13081	109	239	
13002	43370	A	13082	2	88	
13003	43371	A	13083	2	178	
13004	43372	C	13084	278	460	
13005	43373	C	13085	50	217	
13006	43374	A	13086	3	251	
13007	43375	A	13087	1	759	
13008	43376	A	13088	2	604	
13009	43377	A	13089	1	558	
13010	43378	A	13090	3	1055	
13011	43379	A	13091	1	466	MDKFLDTYTLPRLNQEEVESLN RPMITGAEIVAINSLPTKKSPPGD GFTAIFYQRLISNFSKVSQGYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGGRINIVKMAILPK
13012	43380	A	13092	2	848	
13013	43381	A	13093	458	625	
13014	43382	A	13094	482	745	

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13015	43383	A	13095	1	742	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGFNIRKSI NVIWHINRTKDKNHMISIDAE KVFDKIQQPFMLKTLNKLIGDG TYLKILRAIYDKPTANIILNGQK LEAFPLKTGTRQGCPSPLLFNI VLEVLAIRQEKEIKGQLGKE EVKPSLFADDVIVYLENPIISVQ NLLKLISNFSKIKYLGQLTRNV KYLKFNKYKSLLEIKEDTNK WKNIPCSWIGRINIVKMAILPK
13016	43384	A	13096	1	1458	
13017	43385	A	13097	2	1624	
13018	43386	A	13098	1	1095	
13019	43387	A	13099	1	2913	
13020	43388	A	13100	2	1887	
13021	43389	A	13101	1	972	
13022	43390	A	13102	1	873	
13023	43391	A	13103	1	1365	
13024	43392	A	13104	1	867	
13025	43393	A	13105	1	591	
13026	43394	A	13106	1	990	
13027	43395	A	13107	1	2109	
13028	43396	A	13108	1	843	
13029	43397	A	13109	1	1203	
13030	43398	B	13110	1	1221	
13031	43399	A	13111	1	1092	
13032	43400	A	13112	1	931	
13033	43401	A	13113	1	1293	
13034	43402	A	13114	1	544	
13035	43403	A	13115	3	718	
13036	43404	A	13116	693	1397	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLKLLISKFSKVSRKYNV QKSQAFLYTNRRQTESQIMSEL PFTIATRKIKYLGQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFIPYTKINSRWIKD LNVPRKTMKTLEESLGNITQDI GIGKDFMTKTPKAMATKAKRA SAQQKKLPSE
13037	43405	A	13117	1	2814	
13038	43406	A	13118	1	1302	
13039	43407	A	13119	1	1542	
13040	43408	A	13120	3	1327	
13041	43409	A	13121	1	1023	
13042	43410	A	13122	1	1448	
13043	43411	A	13123	1	1038	
13044	43412	A	13124	3	1711	

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13045	43413	B	13125	1	1756	
13046	43414	A	13126	1	923	
13047	43415	B	13127	1	1515	
13048	43416	B	13128	1	1560	
13049	43417	A	13129	1	4032	
13050	43418	A	13130	1	2684	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRKLNLTQSRSTPWKLN NLLNDYVWHNEMKAEIKMFF ETNNKNDTTYQNLWDAFAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTSHKASRRQ EITKJRAELKEIETQKTLQKINES RSWFFERINKIDRPLARLIKKKR EKNQIDITIKNDKGDITDPTIEIQ TTIREYYKHYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAIFYQRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIQKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTKNRQTESQLMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNKIEDTNKWKNI PCSWVGRINIVKMAILPKVIYR FNAIPKLPMTFFTELEKTTLKFI WNQKRAIAKSILSQKNKAGGI TLPDFKLYKATVTKTAWYW YQNRDIDQWNRTEPSEIIPHIYN HLIFDKPEKNKQWGKDSL FNK WCWENWLAICRRLKLPFLTP
13051	43419	A	13131	1	1149	
13052	43420	A	13132	127	329	
13053	43421	A	13133	1	1132	
13054	43422	A	13134	1	1020	
13055	43423	A	13135	803	2009	
13056	43424	A	13136	1	1944	
13057	43425	A	13137	1	1282	
13058	43426	A	13138	1	2423	
13059	43427	A	13139	1	2694	
13060	43428	A	13140	1	1195	

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13061	43429	A	13141	6082	6984	KLAQDRDALSPPLLFNIVLEVL ARAIQKEIKEIGIQLGKEEVKLS LFADDMIVYLENPIV/SAPKSPL RLISNVSVK*GYKINVQKS/QA FLYTNNNTDKQESQIMSELPFTT ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWNIPCS WVGRINIMKMAILPKVNYRFI NSMPSIPIKLPMTEFTTELEKNYF KVHMEPKKSPHCQVNPKTKEQ SWRHQRYLTSNYLQGYSNQK STISMVLVPKQHGTTGTKEIIDQ WNRTEPSEITPHIYNYLIFDKPL LEKNKQWGKGFI
13062	43430	A	13142	193	335	MVEEKLTLPKDEK*KSKQRSY RKTLLQELKNKNEKRNKKNKW QVKTH
13063	43431	A	13143	131	427	
13064	43432	A	13144	1	360	
13065	43433	A	13145	2	376	
13066	43434	A	13146	1	360	
13067	43435	A	13147	2	376	
13068	43436	A	13148	3	469	
13069	43437	A	13149	224	410	
13070	43438	A	13150	478	675	
13071	43439	A	13151	32	161	
13072	43440	A	13152	1	1671	
13073	43441	A	13153	1	1656	
13074	43442	A	13154	62	1295	
13075	43443	B	13155	149	320	
13076	43444	A	13156	12	89	
13077	43445	A	13157	28	417	
13078	43446	A	13158	2	440	
13079	43447	A	13159	190	553	EIVREGASFIRHLRWSRHRKC RFSVKTLTGEDPSTLEVEPS/DT IE/NVKAK/IQDKEG/PPDQQR/L/ VSFAGKQL/EDGRDSLGSY/NIQ KGSLLHPCV*DFRGGAKKKEE ESLYTTSRDK
13080	43448	A	13160	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVFIPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRG VVIPTTSRFSNPIWPVQKTDGS W*TAADY

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13081	43449	A	13161	5	405	HCCGIPHSIAEQDTYFMAKEV WQWAHAHGIHWSYHVPHHLE AAGLIEQWNGLLMSQLQHQLG DNTLQGWGKVLQKVYYALNQ RSIYGTVSPIRIHGSRNQGVVE EVALLTVTPNDPL/GKY*L.PVPV TLHSDR
13082	43450	A	13162	138	387	
13083	43451	C	13163	184	297	
13084	43452	A	13164	1	430	
13085	43453	A	13165	1	867	
13086	43454	A	13166	35	601	CLSRRAAPVYLASMSGRGKGTG G/KARAKAMSRSSRAGRPSQ VGR/VHRLLRKGHYAERVGR QPCCYLG*CMeyLTs*ESWS MAGNAARN\KKTRIPIRHLQ LAIRNDEELNKLA WAALTIAQ GSR/VLPNIQARCCGPR*TSATV GPKAPSGGEERATQASARSTK RARAAAGRPSVPMPPQRP
13087	43455	C	13167	11	313	
13088	43456	B	13168	1	552	
13089	43457	A	13169	1	621	
13090	43458	A	13170	55	296	
13091	43459	A	13171	959	1182	WVYLF*PSCKGVIYP*AAGFESI FWWVTINKNIDWINIYYNQ QFMNYTRDAVKGIAEQLGTNC QMAWENRIALDMILAEGRGVC IMIKTECCAFIPNNTAPNGSITK ALQGLTALSNEASSSGVNDPF TGWLEKWFGKWGITASILTSL TAVMGVLILVGCCVPICGLV QRHRGPPLVVIETKPLGLERLA GLPVGHALKLSGIQATPQNGE NADRREAFPAAS
13092	43460	A	13172	1	540	
13093	43461	A	13173	2	142	
13094	43462	A	13174	42	384	
13095	43463	A	13175	102	329	
13096	43464	A	13176	1	1257	
13097	43465	A	13177	1	378	
13098	43466	A	13178	1	1143	
13099	43467	A	13179	1	481	SDSELNRPVMTMKNFPVFTSDR SKNRKRHFNAPSHVRRKIMSSP LSKELRQKYNVRSMPIRKTDEV IQVYVRGHYKGQIQGGSPRCTR KKYVIYIERVQREK\ANGTNC TWGISPKARWLFTRLKLDKDR KKILERKAKSRQVGKEKGKYK EELIEKMQE

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13100	43468	A	13180	39	556	AAAGYFAEDCEASCVCVKHPP SVKKARCFLSELIKKPSGGSVTL SESTAIISHGTTGLVTWDATLYL AEWAIENPAAFTNRTVLELGSG AGLTG/VAICKMYRPRAFIFSDC HSRVLEQLRGNVLLNGLSLEAD ITANLDSPRVTVAQLDWDVAT VHQLSAFQPDVVIAADVLY
13101	43469	A	13181	46	231	
13102	43470	A	13182	1	1503	
13103	43471	A	13183	3	340	FFFANTFYCVFNVLVNAPLRF SLPSTQSLKLRDSSDSELRRD ILQKVRIPESLGLMTLPPESLRK T*EKNRRCACTL*K/TPVQRTKP LSQHCRVWVWAPPTAPALSFSTK
13104	43472	A	13184	2	594	
13105	43473	A	13185	1	1470	
13106	43474	B	13186	79	1355	
13107	43475	A	13187	248	540	
13108	43476	A	13188	386	1388	
13109	43477	A	13189	386	1334	
13110	43478	A	13190	3873	4070	
13111	43479	A	13191	146	510	PPCAVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAWPKIPFLGIREAKN PRSENTRLTT
13112	43480	A	13192	21	95	KCSSNGAPDAVHE*DLPWTPGP AC
13113	43481	B	13193	1	477	
13114	43482	A	13194	228	935	PLSSSMAAELEFAQIIIVVVTV MVVVIVCLLNHYKVSTRSFNIR PNQSRREDGLPQIMHAPRSRD RFTAPSFQIRDRFSRFQPTYPYV QHEIDLPTTISLSDG/EEPLLYQV PCTLQLRDPQQMELNRESVRA PPNRTIFDS/IDLDIAMYSGGPCP PSSNSGISASTCSSNGRMEGPPP TYSEVMGHHPGASFLHQRSN AHRGSRLQFQQNNAESTIVPIK GKDRKPGNLV

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13115	43483	A	13195	526	1629	FYSFDSARGEAPRPWRVRGLEGRVELGQQLGLLTLGPAPFPGGLGTQQRVGLPGPAGPGAGEGQAGPAEAGQVPVGGLADEAVEHGVGDVAEAGEQEGEVVGVENALGEVAAGLPDAAHQQQHVVGQEAQGQEDDHGAHQPLDLVLAALLGAVAPAHGAQDALVGRQQQADGEEEA/LPGSGSS*WHAAMPGWGSAQSTRGAGSRPR*PPRASGSRCSWAAPWR*PR*RRRPPSGSGTGGSGRDPQPGSGRPTMQQRKPTLM*MFYRRTPTGRTGRRETSCRAAARTAAARRASRCRRGRPPSGCTGTRPARSGP*SAGSEVEGQAVGREAHHQHGNIDHRGQRLVDGMVDGTAHRRGVVCSDDVPH
13116	43484	B	13196	2699	7361	
13117	43485	A	13197	67	1523	
13118	43486	A	13198	1	287	
13119	43487	A	13199	2	563	
13120	43488	A	13200	96	401	
13121	43489	B	13201	1	480	
13122	43490	A	13202	1	924	
13123	43491	B	13203	13	1512	
13124	43492	A	13204	1	402	
13125	43493	A	13205	609	803	RDPRNPSSA\FQAGGIALMLITRGEDLTGGVIHQYPPGGMNLWMQGTAGNQRRRAENAAQQQ
13126	43494	A	13206	3	526	VTETALTLPYLVAKHGYFLPQDLAKRTETMNWLFWLQGAAPFLGGGFGHFYHYAPVKIEYAINRFTMEAKRLDLVDKQLAQHKFVAGDEYTIADMAIWPWFNGNVVLGGVYDAAEFLDAGSYKHVQRWAKEVGERPAVKRGRIVNPTNGPLNEQLHERHDPDFQNTNENNRQG
13127	43495	A	13207	1	250	
13128	43496	A	13208	1	489	
13129	43497	A	13209	209	601	
13130	43498	A	13210	1	96	
13131	43499	A	13211	1	1110	
13132	43500	A	13212	1	595	
13133	43501	A	13213	1	240	
13134	43502	A	13214	1	675	
13135	43503	A	13215	1766	1957	
13136	43504	A	13216	1	426	
13137	43505	B	13217	94	3238	
13138	43506	A	13218	1	2370	

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13139	43507	A	13219	1	2796	
13140	43508	B	13220	43	566	
13141	43509	A	13221	1	903	
13142	43510	A	13222	3	110	
13143	43511	A	13223	2	755	
13144	43512	A	13224	1	1338	
13145	43513	A	13225	1	807	
13146	43514	A	13226	1	918	MARADTVSVPMFMGLAAKPC WRDTEPNTGYRGPHVNRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDAC/LSNAILVHNKKGPP LADGIVITPSHNPPEDGGIKYNP PNGGPAVPTSLKWWKTGPTH WPMA*KA*SVSPARRSDGIRSKN DVIDTSDDDM**QCLSRSSNG HPGAKVANLVPKTTTFIDGVDQT SFFLGTNGQSNRKAHEYFLNGK LAAVRMDEFKYHVLQQPYAY TQSGYQGGGTGTVMQTAGSSV FNLYTDPQESDSIGVRHIFMGV PLQTEMHAYMEILKKYPPRAQI
13147	43515	A	13227	1475	2904	FWRAAAPIDCWRSQAVKKQH VEVTQLDWTTPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGGTGT MQTAGSSVFNLYTDPQESDSIG VRHIFMGVPLQTEMHAPGLPLA SSMKRWIRRTGFIKGKEQFED VVPVLGSKVNGVQFNALVAD SLGISQIRCRCAIFLTVVFPVLH KQAFDLISLLQQPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFET LVQGSPLHQAQVAVDERPH ANRFLPPDEIEQSLNGVHYQHH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRILTRSLOQLRQ LAWPQQQGRYPITYHLFLGVI
13148	43516	A	13228	215	525	LAWARRCRLLAKATSLIRAPS SEMRASTPCRQRRPSGYSWY GRSPRAVLEGLRVGAHLSTRAN CPWPSR/SQVVELIPDGPVFLD FTKIPGRDTQNEHIVLLH
13149	43517	A	13229	1	942	
13150	43518	B	13230	1	1201	
13151	43519	A	13231	685	921	

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13152	43520	A	13232	2	251	
13153	43521	A	13233	2	100	
13154	43522	A	13234	5	1093	
13155	43523	A	13235	2	482	
13156	43524	A	13236	1	2496	
13157	43525	A	13237	572	912	RCRPDKAFTPHPAIGARCLMRR LRVLSCLQPLPNVGWIRRLRRIR QFSAPDEGAKCRVAIQ/DFDA QYGRFLEVTSGAQQRFQTD*K HAAALPFFFPSSAYSLAAISVVF GFR
13158	43526	C	13238	5	127	
13159	43527	A	13239	1	444	
13160	43528	A	13240	17	261	
13161	43529	A	13241	173	397	
13162	43530	A	13242	169	421	LKPKNLDEKLLPASSSSCRIWA TSPVHHLWQVLKKILFGWNP KSPRCLS/TRQAMFSLSKKASLP WTIAARSADQRCRTIAEL
13163	43531	A	13243	17	744	RPHQEORAGCGVNALSSLRSA TAVGMIRASVASG/DRAPIAG CGVNALSGLHRHFIEVTCTHFL LVRYEGIAIFRGGKFRLHLFLN VVLHTLALGIGVCQVKHVEPH AVDTCQGDELELVAHIRQLLE AGNSFVVEVYLPVERRRAVISQ QFARIFRVDSLCKATRFQIRRG RSHQTGQHMGIIRRVDAAHAD DRRTSGRVPPLIQVCFAHSSEA VVVVDVDVDVDVDVDVIGAV
13164	43532	A	13244	954	1104	
13165	43533	B	13245	54	1169	
13166	43534	A	13246	35	3066	VGHSTRPAASGPAAGIGRSPA RLVQQPQORSLAKPLNRPAAQR GLLPQRRHPKRTKRRKQAQN PQKRLPHRPQVRRRRHHRRLL QKMRRPDKRQORRAAPRRHPR RRQRLLA VRRRQLRAKVRNRP RQRAPRQQLNGQRILHPPWRLR MQVRRKRG*YSSAVRPTVRLK RWRQRQRQ*NQPMTMQRNV RKTRTALIYP/YKGCFLNNINAV SKDTFADKRGMRVYRVNAPAG ATSGKYYPPVVMRSAGSFHI
13167	43535	A	13247	1	2919	

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13168	43536	A	13248	1	3211	MEFTSLTPDDLRLVLELYRTPFS DGYVFHSMQFHIFDLLKSGQN VVLASPTSMGKSAIVDSLLGMG TLKRLVLVPTVALADETRRRL QERFGDRYQIIHSSQVCHSDQ AVYVLTQERVNERDDIVIDLF VIDEFYKLAFRQLKSGDIDHQD ERVIELNIALSKLLKVSRQFYLT GPFVNSIRGLEKLGYPHTFVST DFNTVALDVKTSASKRMTTKP SSKRWGKSRTCVDADHIKNGIG LHFGALPRALQQYT
13169	43537	A	13249	486	3882	LRLRGEALPVASGCLANATDTP AGTTLWATERHAVQ**TCEA DTLGSCGYAAKPCLSPPVAVWQ MLLTRLLEQHYGLTLNDTPFSD EPVLTAPIDAAALRGIEFGKFQ GNMVGDIIECGSDVTDYAVG DSVCGYGPLSETVIHNAVNNYK LRKMPQGSSWKNAVCDPAQF AMSGVRDANGARRGFWWGGL GAIRVQLAFKWLNAAGRLPGG GLGGPIPSAHRCDIARRHGAD FCLNPIGTDVGKEIKTLTG
13170	43538	B	13250	1	1116	
13171	43539	A	13251	729	985	SAPPQLAPSLPDRATDPDTCWP PG*RP*RYLPSRQIDCFNTRFRLL QRLTASQCAEAVDVAFRLTV QQTPHFRCAQLRQRAFRID
13172	43540	A	13252	395	605	
13173	43541	A	13253	1	1140	MIYVFVTVKHRNDHFTKNTLA SYRGRTLLGLTFKGVYHLYKD ETYLQSGKGHTIQEVRIKGL NNPDLDAAVGEDLAQQLRDEL ELVKGASNEFDKELFLAGEITP VFFGTALGNFGVDHMLDGLVE WAPAPMPRQTDTRTVEASEDK FTGFVFKIQANMDPKHRDRVA FMRVVSQGYEKGMLKRVRT AKDVVISDALTFMAGDRSHAY PGDILGLHNNHTIQIGDTFTQG EMMKFTGIPNFAPELFRIRLK DPLKQKQLLKGLVQLSEEGAV QVFRPISNNDLIVGAVGLQFD VVVARLKSEYNVEAVYESVNV ATARWVECADAKKFEFKRKN ESQLALDGGDNLAYIATSMYV LRLAQERYPDVQFHQTREH
13174	43542	A	13254	1	1495	

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13175	43543	A	13255	372	1365	IRYFENRGLFAHCATRTGQFPP HCILASYKCGEQPDSSSNHPRN LFVWRSNLLGSSG/KGHEYMQ KYL LGTESGIQGEELGASDGIKP EEVEWQTA AIEGKLDLVLTLDF RMSSTCLFSDIVLPTATWYEKD DMNTSDMHFPFIHPLSAAVDPA WESRSDWEIYKGIKAFSQCVCV GHLGKETD VVLQPLLDHSPAEL SQPCEVLDWRKGECDLIPGKTA PNIVAVERDYPATYERFTSLGP LMDKLGNGMDLTDYANMALSI PSANTDIWNLEQDVTGTRLTNS RHGLADNGGAWSYFGGNFN GDNGTINYDQDVNGIMGVVD KIDGNDG
13176	43544	A	13256	3	1444	
13177	43545	A	13257	61	1058	LPYLIALLARAWFNGLLTSRTR LYIKGNIGIVL PKLQEMVADVS HHFPLRLPAPT PKALYSPCEIRH LAINVNLEYDPTAAFRNQVVHF DFRKL DVFSFGENQNC LVGNV DLLYRNSWNEVRTLHFNGEQS MIEALKTILGKMHQDAAPPDSV EVFCYSQHLRLIRTRVQQLVS ECIELRLSSTRQETGRFKALRVS GQTWGLFFERLNVSVQKLENAI EFYGAISHNKLHGLSVQVETNH VKLPA VVDGFASEGIIQFFFEET QDENGFN IYILDESNRVEVYHH CEGSKHEELVRDVS RFYSSSHDR FTYGSSFINFNLD PPLYLARVSI
13178	43546	A	13258	1	1133	
13179	43547	A	13259	2	240	ISSARHFGALACTLELGKALT GQNDLRQFAVTA SAIAALL/SR HSPSFEMHMASD TLNFMPEFK GTLLAQDGEERFTVTH
13180	43548	A	13260	1	358	LPFLPSGLRGLA AENKIRRP GSFLGPCCGLRGKL V/ISAALM STTIPISRVQGLLQFLNSKSPISR AERSWSTFGASA AFLTTLASLL FLFPPLAISSLANSFAKVFPPTPC AGSP
13181	43549	A	13261	1	1635	
13182	43550	A	13262	1	1363	
13183	43551	A	13263	5	249	
13184	43552	A	13264	15	280	
13185	43553	A	13265	6	363	

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13186	43554	A	13266	78	346	TRYAMLTRHDNHLKSFYLARG RYRADFHAPETNTGERCYRYK PLPYWLE*RRGRNRYPALQ*TM FLPADGPARCLSRQAAILKESV LPK
13187	43555	A	13267	568	831	ELQRHVLVVFAGFWIVKNSRN LFLVCAEHKRSVVKGLLRQQ GQGFWFHFQDGFAVEVGNAN VIGSE*IVFGIVFPHRERCLVDK
13188	43556	A	13268	3	419	
13189	43557	A	13269	1	561	
13190	43558	A	13270	1	741	
13191	43559	A	13271	2	1040	
13192	43560	B	13272	1	1974	
13193	43561	A	13273	2111	2340	EVFIRDKLMERRNRRTRTEKA /RDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPVKVLQSQCI
13194	43562	A	13274	470	813	KTTSPAKLFNACRISLLASAEV NPNISAYLATWISQIPSCSRVP SDFLIWSNTRYRIR*SRERLVG EAV/AAAAADGVTFSVPVTPHT FRHSYAMHMLYAGIPLKVLQS LMGH
13195	43563	C	13275	440	1180	
13196	43564	A	13276	1	1290	
13197	43565	A	13277	1	1036	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPKARKITRRWRIG EAADLVGVSSQAIRDAEAKGR LPHDPMENSRRDRFEQGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMLVKNVRETDEVG KDPRPLPYLGHDEPYTFDINLS VNLKSMVVGDTMDGQEPKQ MGAWGPLSLKAMGFFIRGYG FFTPFGRITLPLGFGSTPPFTPL LTKTIGVFILDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA GAAAAADGVTFSVSTPHTFR HSYAMHMLYAGIPLKDLQSLM GHKSISSTEGYTKDFSLDVG/AR HRVQFAMPESDAVAMLKQLF
13198	43566	A	13278	366	672	RNGTHPRYIEAVPWGALPAD/G VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLALRELQQA VHAGLPQAKILFDGGSEIGKIPH IVLYKPVQCSSLWAFVH
13199	43567	A	13279	2602	2976	
13200	43568	A	13280	982	1347	
13201	43569	A	13281	1	780	
13202	43570	A	13282	568	891	

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13203	43571	A	13283	1	718	MKEKPSSPRQYSYSLSSMILLG GGESWNLRLADQLRIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEA VAAAA ADGVTFSPVPTPHTRFSYAM HMLYAGIPLKVLQSLMGHKSIS STEYVTKV/FALDVAAPHPESTP VHLPSRENKIPPPIMRIPCGLPTS PIEQKQGISATGTQWRRLKQE TRLSSVSARLMSYVGVMC
13204	43572	A	13284	1	496	AMFGFFIRGYGFFTPFGRTLFLP FGGSTPPFTFPLLTKTIGVFILDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEA GAAAAADGVT FSVSVTPHTFRFSYAMHMLYA GIPLKDLQSLMGHKSISSTEGYT KDFSLDVGARHRVQFAMPES DAVAMLKQLF
13205	43573	A	13285	2	545	
13206	43574	B	13286	1	735	
13207	43575	A	13287	1	1599	
13208	43576	A	13288	583	1005	
13209	43577	B	13289	31	1239	
13210	43578	A	13290	1	1023	
13211	43579	A	13291	1	933	
13212	43580	A	13292	1	1278	
13213	43581	A	13293	1	705	
13214	43582	A	13294	2	893	
13215	43583	A	13295	88	429	
13216	43584	B	13296	1	1419	
13217	43585	A	13297	1	2784	
13218	43586	A	13298	163	416	RNGTHPRYIEAVPWGALPAD/G VTFSPVP/TPHTFRFSYAMHML YAGIPLKVLQSLRALRELQAV HAGLPQQA KILFDGGSEIGKI
13219	43587	A	13299	740	1431	CCQTLPVFHPHPSHLGPRPCPP TH/HLPSEHRS/LFLEAACHDS LEPLNLSSGSKTSPSPLPKAKK PKGLEISA/RPAGALRHRRLHR PQQSPPLGIPHPSL/LTAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEA VAAAAADG VTFSPVPTPHTRFSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13220	43588	B	13300	1	858	
13221	43589	B	13301	1	1098	

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13222	43590	A	13302	1	1047	MNRQLSDSYTEDTKPEPSDVTTS ETRSPPGSAKTTMIDTLKKLQ DVLKTEDSKNPTKSAADLLEQ YVKATGPHEILQKATKTMEMI MIVEEKASDELQDPPELQQRVI HSVRGKPGLVKQRTQEITRLR LAGLTVSSPLKRSHSLAKLGSL TFSTEDLSRPPGPPGPPGLHP GPPPRRPPKLPAPPGCSVHC CHYPLHFVVSPLGFGYCSLMRI QIVFVTFVHHDSALLPLDASL APEALQNFQRYTGQIHVIRIGM AERMWCDNRNRHTVSSSGGN RLPNPAPLPNPGVL SAPPNLIQR PKADDTSAATIEKKATATISAK PQITNPKAEIT* NPRVWQGSWI GEAVAAAAADGVTFVSPVTPH TFRHSYAMHMLYAGIPLKVLQ SLRSQ*SVRGKPLVKQRTQEI ETRLRLAGLTVSSPLKRSHSLA KLGSLTFSTEDLSRPPGPPGPP PPGLHPGPPPRRPPKLPAPPP GCSVHCCHYPLHFVVSPLGFGY CSLMRIQIVFVTFVHHDSALL PLDASLAPEALQNFQRYTGQIH VHRIGMAERMWCDNRNRHT VSSSGGNRLPNPAPLPNPGVLS APPNLIQRPKADDTSAATIEKK ATATISAKPQITNPKAEITRFPCL
13223	43591	B	13303	1	1185	
13224	43592	A	13304	529	774	
13225	43593	B	13305	1	1089	
13226	43594	A	13306	712	1024	GVESNLVVVVVALCHRLIYLVW GTRTVRTWIGEA VAAAAADGV TFSVAVTPHTFRHSYAMHMLY AGIPLKVLQSRVVALDVAARH RVQFAMPESDAVAMLKQLS
13227	43595	A	13307	556	1040	
13228	43596	A	13308	1	984	
13229	43597	A	13309	95	428	
13230	43598	C	13310	1	426	

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13231	43599	A	13311	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIERVQLPQSYQLY YFELAIPIVGYFYPGFSFSTARIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHSISTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVRETDEVG KARLTWIGTINVVCAADVLI PTPAELFDYTSALQFFDMLRDLL LKNVDLKGFEPPDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
13232	43600	A	13312	1	1593	
13233	43601	A	13313	1	2536	
13234	43602	A	13314	887	1205	RPEKAR/IWGVTDRTVVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAAR RHRVQFAMPESDAVAMLKQLS
13235	43603	A	13315	79	351	
13236	43604	A	13316	1	2320	
13237	43605	A	13317	187	798	
13238	43606	A	13318	2089	2610	
13239	43607	A	13319	1	1407	
13240	43608	B	13320	154	3682	
13241	43609	A	13321	1	1206	
13242	43610	A	13322	1	255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \=possible nucleotide insertion)
13243	43611	A	13323	3058	3160	GSAA*LPPLPAAFSGCWLSQLRHPDLHV*NEIYHLLH*KSFTSC*HNLSS*PRYPYLSSEVLW*CLSFISKI*SVTMP*DLISLW*KLEPLTCRSTSHFRQKLAQ/RLP/AYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEKARIWEVTDRTVRTWIGEAVAAAAADGVTFSVPVTPHTFRHSYAMHMLYAGIPLKVLQSLMGHKSSISTEYVTKVFDLDVAARHRVQFAMPESDAVAMLKHYPEINALALYLKCGTEWIC
13244	43612	A	13324	1	1812	
13245	43613	B	13325	1	1776	
13246	43614	A	13326	583	751	
13247	43615	B	13327	826	2097	
13248	43616	A	13328	1810	4163	
13249	43617	A	13329	686	2939	
13250	43618	A	13330	1085	1690	SYFIMVKVGTSYVPINVSFSPKVGPASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRUIYKARIWEVTDRTVR/TWICRGLPAAAAADGVTFSDPGPPHTFRHSYAMHMLYAR*YR*KFLQSLMGHKSHPINGKATPKVFGPGMGLARA/HRGAGWQWPKSDAVG\MPKQLSLRINALGLYMETGKPEGIMLFFGC
13251	43619	A	13331	3	327	
13252	43620	A	13332	3	337	
13253	43621	C	13333	167	413	
13254	43622	A	13334	1	1256	
13255	43623	A	13335	1	1078	
13256	43624	A	13336	3	976	
13257	43625	A	13337	1	1004	
13258	43626	A	13338	2	291	WRKIYEANGKKRKRLQSL*SLMKQTLNQQRSKETKKASA/SMRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWVG RINIVKMAIPPK
13259	43627	A	13339	1	2022	
13260	43628	A	13340	1	2262	
13261	43629	A	13341	5	283	
13262	43630	A	13342	1	1245	
13263	43631	A	13343	1	1203	
13264	43632	A	13344	1	687	
13265	43633	B	13345	1	1371	
13266	43634	A	13346	1	2241	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13267	43635	A	13347	1	832	LKKCIKTP EIPSKHVRNWVPKV LEQRRQGLETYLQVASITLIPKA DEDTPKKKTTDKNSWTGTDK VFNKILEIKFSSILKRLYWPVLE VLARAMRQEKEIKGIQLGKEEV KLSRFADDMIVYLENPVSAQN LLKLISNFSKVSQYKINQVKSQ AFLYTNNRQITESTQIRIKYLGIG LTRDVKDLFKENYKPLKEIKE DTNKWKNPCSWVGRINIVKM AILPKRYPFCQLCHQSAISTTKG VFTSILPLLMEQLVSGRSCPSV AWSSMECTTV
13268	43636	A	13348	1	1314	
13269	43637	A	13349	1	843	
13270	43638	B	13350	1	1011	
13271	43639	A	13351	1	173	
13272	43640	A	13352	1	323	
13273	43641	A	13353	3	2020	
13274	43642	A	13354	1	1473	
13275	43643	B	13355	1	636	
13276	43644	B	13356	1	456	
13277	43645	A	13357	1	619	
13278	43646	A	13358	1	1293	
13279	43647	B	13359	79	1041	
13280	43648	A	13360	3	718	
13281	43649	A	13361	1	612	
13282	43650	A	13362	1	992	
13283	43651	A	13363	1	1236	
13284	43652	A	13364	1	1071	
13285	43653	A	13365	359	1250	KLP MGVA VVKLLHLPKVIIVFW LASWMMSRWLHYPDWVTIIAQ QVLMNVVSVMQADCRMNLEI FLRWLMRKIFHVRLLPAVSTPP NCLNQLLLFLLTPVNYLPGQVM HFKKPLQIKRNYLSSRHITFMS RKKLGVSGYKIHVQKSQAFL SANSQGOTESQIMSELPFTMASK RIKYLGIQLTRDVKDLFKEKYK SLLNEIKEDTNKWKNNPCSWV GRINIMKMAILPKVIYRFNAIPI KLPMTFFTELEKTTFFIWNQK RAHIAKSNLSQKNKAGGITLPD FKLYYKATVTKIT
13286	43654	A	13366	1196	2132	
13287	43655	A	13367	1	2271	
13288	43656	A	13368	2	1105	
13289	43657	A	13369	1	2117	
13290	43658	A	13370	1	1447	
13291	43659	A	13371	1	1669	
13292	43660	A	13372	1	2823	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13293	43661	A	13373	1089	2539	
13294	43662	A	13374	1	1787	
13295	43663	A	13375	1205	1207	
13296	43664	B	13376	1	2745	
13297	43665	A	13377	1	2063	
13298	43666	A	13378	1	4380	
13299	43667	A	13379	1	3347	MGDFNIPSLDRLSTRQKVNKD TQELNSALHQADLDSYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEITNYLSDHSA IKLELRINKLTQNCSTTWKLN LLNDYVWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKA VCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQEI TKIRAELEKETQKTLQKINESR SWVFERINKIDRLARLTKKKS EKNQIDAINKDK
13300	43668	A	13380	1	2367	
13301	43669	A	13381	1	1116	
13302	43670	A	13382	1	1095	
13303	43671	A	13383	670	1500	QTESSTSKSLSTMIKWASSLG WQGWFNIRKSINVIQHIKGIQR QKPHDYLNRCKSL*QNSTTLH AKNSQ*IAQNLLKLISNFKVS GYKINVQKSQAFLYTSNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNI PCSWVGRINIVKMAILP KVYIRFNAIPIKLPMTFFTELEK TTLKFIWNQKRAHIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNM CYRSMEQNRALS YYVAYLQPSDL
13304	43672	A	13384	441	3131	
13305	43673	B	13385	1	5688	
13306	43674	B	13386	916	2165	
13307	43675	A	13387	1	1529	MDPPAGAARRLLCPALL*LPAG *PLRPRLAGAAPAGTALLHER AMPL*LRPGLHDVHGVDPDL
13308	43676	A	13388	1	714	
13309	43677	A	13389	3	457	
13310	43678	A	13390	2	492	
13311	43679	A	13391	3	1201	
13312	43680	A	13392	1	309	
13313	43681	A	13393	2	1073	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
13314	43682	A	13394	3119	6984	CIVKHAAMRSAMTSLAARITVL NPTRATTPTNT/RVADDQGFRLRQ WSKVAKERKLQRLYLIGEPSAEA VAAQMPDLILISATGGDSALAL YDQLSTIAPTLIINYYDDKSWHPR LSFNKADEITTVCFSKSLAN GIPMANILFPTSVIATQQTQHFR FVDDFNAQFLRFASLDPAA SPA ITISGKATLEIPGTGVFYAAALE KKLNKPGQTTDFGRFTLLPTC CLGNCDKGPNNMIDEDTHAHL TPEAIPELLER
13315	43683	A	13395	3	587	
13316	43684	A	13396	1	315	
13317	43685	A	13397	430	636	
13318	43686	A	13398	1	84	
13319	43687	A	13399	1	1647	
13320	43688	A	13400	1	2652	
13321	43689	B	13401	1	1494	
13322	43690	A	13402	1	750	
13323	43691	A	13403	1	513	
13324	43692	A	13404	1	2254	
13325	43693	A	13405	1	746	
13326	43694	A	13406	3	428	LGDDFVRAANIILHCEGKVVS GIGKSGHIGKIAATLASTGTPA FFVHPAEALHGDLMIESRDV MLFISYSGGAKELDIIPRLEDK SIAL/GKPTSPLGLAAKAVLDIS VEREACPMHLAPTSSTVNTLM MGDALAMAV
13327	43695	A	13407	1	1431	
13328	43696	A	13408	943	2481	
13329	43697	B	13409	1	783	
13330	43698	A	13410	3	729	
13331	43699	A	13411	1	843	
13332	43700	A	13412	3	128	
13333	43701	A	13413	1	136	
13334	43702	A	13414	1	492	
13335	43703	A	13415	3	619	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13336	43704	A	13416	1	1600	GQACHASSSPLKSGRGSPPNFEI LYGPIFEDSLAPD*PKVIAGQIT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLDFALYFFHNYQA LLAKGSGPYFYLPKTSQWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDIELHALR DHIVGLNCGRWYIFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTCRKGAFAMGGM AAFIPSKDEHNNQVLNKKVA DKSLEANNHGDGTWIAHPGLA DTAMAVFNILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKQSQNLWKFA VYSGLRHGELAAALAWEDVDLE KGIVNVRNLTILDMFGPPKTN AGIRTVTLLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFA SQMGHETAQMVVEIYGMWID DMSDEQIAMLNARVM
13337	43705	A	13417	2	278	
13338	43706	A	13418	3	662	GHLWIRIDLSQSAVSHSVKELE NHTGVRLDRITREVVLTADG QQIALRLERLLDELNSTLRDTG RMGQQLSGKVRVAASQTISAH LIPQCIAESHRRYPDIQFVLHNR PQQWVMESIRQGDVDFGIVIDP GPVGDQLQCEAILSEPFLLCHRD SALAVEDYVPAALPLPEGSPLVV KRITPVVERQLMLVRRKNRSL TAAEALWDVVDRDQGNALMAA
13339	43707	A	13419	1	646	GQQLSGKVRVAASQTISAHLIP QCIAESHRRYPDIQFVLHNRPO QWVMESIRQGDVDFGIVIDP VGDLQCEAILSEPFLLCHRD LAGGDYVPWQALQGAQLVLQ DYASGSRPLIDAALARNIQAN IVQEIGHPATLPPMVAAIGISIL PALALPLPEGSPLVVKRITPVVE RQLMLVRRKNRSLSTAEEALW DVVDRDQGNALMAIGRE
13340	43708	A	13420	1	1068	
13341	43709	A	13421	1	381	
13342	43710	A	13422	3	938	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13343	43711	A	13423	595	1630	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESQGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESQGDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLES GHYDHDYEFELGTR FRAVIIKLCNGDSLRFHMTSVY ALVKCFHEGDP LHKGTGCQHLIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVEMLLREAGKAGFC RFRNHHTGFSPAGANQRGPL AATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGNSYDHDYEFELGTHQ RLGAVARI VGDDLNLRRDV VDARAGDVDQHAHAKEKGDFR
13344	43712	A	13424	1	1395	

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13345	43713	A	13425	1307	1992	DKLNPVAHQKAYLAQSSQCHP QNA RL VQHTQIRILPISEPPSNRI FACWGKPAWTACCN/FSQGGQA VKG NQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV K R K T T L A P N T Q T A S P R A L A D S L M Q L A R Q V S R L E S G Q D F A D F G T T I K Q D F R L L G Q T S V D R L L Q L S Q G Q A V K G N Q L L P V S L V K R K T T L A P N T Q T A S P R A L A D S L M Q L A R Q V S R L E S G Q L K H K E V E S P N R P I T S S E I Q V L I K L S P I K K S P G P D G F T A E F Y E R Y K E E L V P F L L K L F Q T I E Q E R L L P N S F Y E A S I L T S K P S R D A T K K D N F R P T S L M N I Y A K I L N K I G Q T E S S T S K S L F S T I K S V S S P E C K A G S T Y A N Q D F A D F G T T I K Q D F R L L G Q T S V D R L L Q L S Q G Q A V K G N Q L L P V S L V K R K T T L A P N T Q T A S P R A L A D S L M Q L A R Q V S R L E S G Q E T T P W S P F S D P V L A F D Y K V F M A F V Y N V V R V S Q R M V V A G C I S A F N D K L L N D L I C F P V A P V S S K Q I F P S D V K V A E P D H S C V S S Y R I G S M A P N L T L S E M P R H N Y F P A G N S V D H D N E F E L
13346	43714	A	13426	560	844	
13347	43715	B	13427	200	1519	
13348	43716	A	13428	950	1230	CSWIHDFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQ QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVK NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ

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13349	43717	A	13429	695	1060	FRQRSVAFPTVPNACVSVRSR ERDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQ* AQR N*CRKHRLSIPRK
13350	43718	A	13430	1	1558	MRDIFWVPDICKVMLYL VFFRS MGTPPLRAVAMGLVITSWKIAQ KPRDFADFGTTINQDFRLLGQT SVDRLQLSQGQAVKGNQLLP VSLKTDTKAKNLYLT KAYYGG GTNFFRKESQKLQSAKKRDA ELANGALGHIELNDYTLKKVM KPLITSNTGFAFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMLQARQVSRLESG Q* AQRN
13351	43719	A	13431	391	1676	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQ* AQR N
13352	43720	B	13432	1	1638	
13353	43721	A	13433	1	2430	
13354	43722	B	13434	1	1282	
13355	43723	B	13435	1	1225	
13356	43724	A	13436	350	709	
13357	43725	A	13437	1	2236	
13358	43726	A	13438	548	1698	RSWLRSSLSGSIPIATEISCSTCE ASTSS/VRDFPGVKDLTFQWHD RLIFAIALRLGRSACGVTFHKEQ LGTVKVLRGTISQFARQRAAG QLFTHHFFGRHTALGAGNRH LRQQFSRLNVLVQPQDKGIFHH ARNECALTRRETPAFFRIRAVF NSQLSQTQLHIFTARPAGLAS KCRKPPQACYLWDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMLQARQV SRLESGQNIESAKGLHVWDSW PLHNADGTVDEYNGYHVVFAL AGSPKDAADTSIYMFYQKVG NSIDSWKNAGRVFKDSKDFDA NDPILKQDTQEWSGSATFTSDG KIRLFYTDYSGEHYG
13359	43727	B	13439	448	1116	
13360	43728	A	13440	97	1636	
13361	43729	A	13441	1	1296	
13362	43730	B	13442	1	2160	

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13363	43731	A	13443	485	865	FIRDFADFGTTIKQDFRLLGGQTS VDRLLQLSQGQAVKGNQLLPV SLVKKRTTLAPNTQTASPRALA DSLMLQARQVSRLESGQS*NSS KTKNTKCLNSINQRLKILSLQK DLMCGTAGRCKTLTEQ
13364	43732	A	13444	816	1194	SLILFLRRRRRAVEKRGKVVWQDS CPNGTTTLTSGAIFLFIREFADFG GTPITQDFRLLGGQTSVDRLLHLS QQGQAVKGNQLLPVSLVKKRTT LAPNTQTASPRALADSLMLQAL RQVSRLESGQ*AQRN
13365	43733	B	13445	1	2710	
13366	43734	A	13446	2027	2934	NPRILPISEPPSNRIFACWGKPA WTACCNFSQQAQVKGNNQLLP VSLVKKRTTLAPNTQTASPRAL ADSLMLQARQVSRLESGQDFA DFGTTIKQDFRLLGGQTSVDRLL QLSQGQAVKGNQLLPVSLVKKR KTTAPNTQTASPRALADSLMQ LARQVSRLESGQSRVHSHSLGP LPTTTTGLSLNQKGGVSGGPG SKEQAEISCLKERKDLGLGLGS TVGILKVKHQGASTKQGHSD LIKILLSDTSLTPAAPMVDSLIA RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWWSGNE RDQELLTEDALDDLPSFLLTGQ QTPAFGRRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDQ MAALSRLGNDYRPTSAYERGQ RYASRLQYMNLLPIFLRWLMR KIFHDEHVPQDQEEPISEITII EEEIPINSIDLGNELYFVKLPKF LSIEPKDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKKRTTLAPNTQTASPR ALADSLMLQARQVSRLESGQP HSTDASATHRKMTLSLADRCST QKIRILPMAGRDPECORTEMIK SSDLMAEIIQEHKEDQLPELEQL EHIGLFSHAEIKAIKKASDLQY RIQERALFKDDFINYVLHEIPLF EQIQRRTIGYSLKHGIRAVKA TIVRALYGRIPAGVVVTRSV
13367	43735	A	13447	1	5240	
13368	43736	A	13448	4733	4753	

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13369	43737	A	13449	299	761	LNTTATLCLLLREARKTLMTH QSTCFIKRDFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN**PVPKEKRRRGDRQE HQQPCRNTEGTALRVWAARDQ
13370	43738	A	13450	3925	4190	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQ*AQR N
13371	43739	A	13451	2	1040	
13372	43740	A	13452	58	350	HLASWVVALVLHWGCVVWTA ESSTSKTRSPFRARSWIGEAVA AAAADGVTFSPVPTHTFRHSY AMHMLYAGIPLKVLQSLMGH KSISSTGVPSSNS
13373	43741	A	13453	1	1290	
13374	43742	A	13454	289	1338	
13375	43743	A	13455	1	732	
13376	43744	A	13456	982	1347	
13377	43745	A	13457	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSPV VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAARHRNFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPIVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEVDV RILLTKYSNSNGSQSPWMEEQI RDAWGSVMVLKNVRETDEVG KARLTWIGTINVVCAADVLI PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEVDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSVM LKNVRETDEVGKPEPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMKLQSL
13378	43746	A	13458	1	780	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
13379	43747	A	13459	116	396	SSVTGRTEKARIWEVTDRTV/R RPWIGEA VAAAADGVTFSP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYVTKVF ALDVAARHR
13380	43748	A	13460	3	514	
13381	43749	A	13461	2	545	
13382	43750	A	13462	1	1110	
13383	43751	A	13463	1	870	
13384	43752	A	13464	1	1422	
13385	43753	A	13465	1	1599	
13386	43754	A	13466	614	1236	TARVAAARRRCQCWGSACGS ALTLPTSSLTLTETPIVQQTRM VVRCPTASLPQWRSPSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVDTRTVRTWIGEA VAAAAD GVTFSPVTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13387	43755	A	13467	1	1023	
13388	43756	A	13468	1	699	
13389	43757	B	13469	1	1281	
13390	43758	B	13470	77	751	
13391	43759	A	13471	1	705	
13392	43760	A	13472	2	893	
13393	43761	A	13473	206	837	CAGAGGIARRRAEKEKALSAV NLDPTSSRLSSTSLPGAPPNPRV AAAGLSRRRPTSPSAGRKS/GR WPRASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVTRTWIGEA VAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYVYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13394	43762	A	13474	1	1416	
13395	43763	A	13475	1	765	
13396	43764	B	13476	1	519	
13397	43765	A	13477	1	2784	
13398	43766	A	13478	1	624	
13399	43767	A	13479	2089	2454	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, ~-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13400	43768	A	13480	740	1431	CCQTLFVFHPPHPSHLGPRPCPP TH/HLPSEHRSFLFLEAACHDS LEPLNLSSGSKTSPSLPPKAKK PKGLEISA/RPAGALRHRRLHR PQQSPPLGIPHPSLUTAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAFAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13401	43769	A	13481	2	2309	
13402	43770	A	13482	1	603	
13403	43771	A	13483	1	762	MVPHSTGKSWNGCDPTSATLD QLVTVFFMKLFSIGDARIPCLGP RSHSYRRSDYYSGTIIHSCRA DYWSGTTAHLRCRSDYHPVPS FILVTSTTNHQPLKPSISEASWN PLFASL/HHLQLITES/W/YMSLA TTVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAFAA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13404	43772	A	13484	1	762	
13405	43773	A	13485	1	615	
13406	43774	A	13486	887	1203	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
13407	43775	A	13487	1	855	
13408	43776	A	13488	1	927	
13409	43777	A	13489	1	921	
13410	43778	A	13490	1	3216	
13411	43779	A	13491	1	1974	
13412	43780	A	13492	1	1221	
13413	43781	B	13493	1	2337	
13414	43782	A	13494	1	1273	
13415	43783	A	13495	1	1251	
13416	43784	A	13496	1999	3237	
13417	43785	A	13497	1	1773	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13418	43786	A	13498	1	633	AQALIAITYGRDRDPGRPLWL SVKSNIGHTQAAAGVAGVIKM VMAMRHGQLPRTLHVESPSPE VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEA VAAAA ADGVTFSPVPTPHTRFSYAMH MLYAGIPL/*VLQSLMGHKSIS TEVYTKVFALDVAARHRVQFA MPESDAGGPGTCACSQQCRL RGSSVSPGRQHPQPHRV
13419	43787	A	13499	101	1943	
13420	43788	A	13500	686	3925	
13421	43789	A	13501	1	2084	
13422	43790	A	13502	734	834	
13423	43791	A	13503	1	1075	
13424	43792	A	13504	1	357	
13425	43793	A	13505	795	1273	SHPFSTDWSTDTGFRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVVSMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLFFLTPVNYLPG QVMHFKKPLQIKRNYLSSRLT FMSRKKLG
13426	43794	A	13506	344	449	SHPFSTDWSTDTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASCMMSRCPHYPDWVTI IAQQVLTPRKDVMSQADCRMN LLEIFLRWLMRKIFHVGFM
13427	43795	A	13507	1197	1511	WHYREPLLRAQLTNPPSGQLV SITKYLQPVVE*AYVLE*QAH HYQLKSVQDQWPVQKQFSSGSD LYQLHPFHVQHLEPCFPRHPE FAPPSTGTESHYYCCIW
13428	43796	B	13508	1	1494	
13429	43797	A	13509	1	554	MTARKARKITRRWRIGEAADL VGVSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVFGRLLRAEDVFPPIGVAA HKGNPDQGTASMYHGWVPLD HIHAEDTLLPFYLGKDDVITYA IKPTCWPLDIIPSCALHRIETE LMGKFDEAQPNLGIGT/N*CRM CC*CADCSHAC
13430	43798	A	13510	1771	2068	DTYSVSWIGEA VAAAAADGVT FSVPVTPHTRHYSAMHMLYA GIPLKVLQSQYPIFKLSYKNPVT QTA WFWFFNRIFGPVPIVNSFS PKVGPGLPGII
13431	43799	A	13511	65	277	

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13432	43800	A	13512	327	748	VHQFHGSLHEGFCAGCGCPAP GTVCDAGGFCFRFRNHHQTGFSP AGANQRGPLAAATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AKSIWCHRNCRW/RVAVVKLL HLPKVIIVFWLAS
13433	43801	A	13513	512	580	
13434	43802	A	13514	2096	2272	EWRNVCGVTGTENVTPSAAAA QPPQSRPFSWILRPF*RP*RKIS TSFIRPLFTFLPA
13435	43803	A	13515	402	2784	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI*HTQNQRSGRSQSD F*RRRNISERSAAAYR*RQLYIR RQPYAERPSHVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIHELNDYTLK KVMKPLITSNTVTDEIERANVF KMGKGYLFTDSRGSKMTIDG INSNDIYMLGYVNSLTGPYKP LNKTGLVLQMGLDPNVDVFTY SHFAVPQAKGNVIVTSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQQGLTWLQVA KRAGLGGGQSGRTVLRERLPN YKNFKGTIQELGQNGYAVSGEI FVVDNRNTVEITELPVRTWTQVY KEQVLEPMLNGTDKTPALISDY KEYHTDITTVKFVVKMTTEELA QAEAAGLHKVFKLQTTLTCNS MVLFDHMGCLKKYETVQDILK EFFDLRLSYGLRKEWLVGML GAESTKLNNQARFILEKIQKII IENRSKKDLIQLMVQRGYESDP VKAWEAQEKCDNLKTCHTSH GSVMAETA VINHHKRNKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGDICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRLS
13436	43804	A	13516	2	199	WRKKSLDIPPLIIPNGIVKNILRH FSQLLNVPIRPFWSWILRPF*RP* RKISTSFIRPLFTFLPA
13437	43805	A	13517	1	1887	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
13438	43806	A	13518	125	828	ECKRHTKLKLPQTIWHVLI/Y NSEKLLVYRKLLQVLTLGYKRS NLGVRLYACCGLLCPAYPQH FAHGYYVDKIPGYGRAGTLTGL HPMQCDNLKTCHTSHGSVMAE TAVINHKKRKNSPRIVQSNLDT EAAYSLSRDQKRMLYLFVDQIR KSDGTLQEHGICEIHVAKYAE IFGLTSAEAILRVFIKHSADMEA ITNGMMNLNRQRHQHLVALRII FAHGENGGEEVVHIGHV
13439	43807	A	13519	504	755	EPCFPAIPEFAPLSTGAESHIIY CCIW*AKYVHQARTL*DQRS*A DHEAYRKTAVRRCSTTQQAWE EQLVHQHILPSSCRYPG
13440	43808	B	13520	1	1980	
13441	43809	A	13521	923	1063	
13442	43810	B	13522	1	1932	
13443	43811	A	13523	383	1383	RKVFFIALKRPAMKKAMNLF LGLSNVRTVHIEGFTVYISTHIS FPISLGYKTRLSFGLVKQKKS PILLEVLAREIQE/KEIKGIQGF KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRKYLGIQLTRDVKDL FKENYKPLLEIKEDTNKWKNI PCSWVGRINIVKMAILPKLSRM HGRPHQPPNAASTLPFKRRSH YGQKSERLSRSGDNRKSHPECR HWQSCAKKSRCLAFTRTVRHT PRSAYLRTTIELLESSALWHV QTRQRIYAPLYETLDPGNRTHCE
13444	43812	B	13524	107	1000	
13445	43813	A	13525	1778	1897	
13446	43814	A	13526	273	421	SHPPFSTDWSTDGTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFSSAS
13447	43815	A	13527	273	697	SHPPFSTDWSTDGTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMSRWLHYPDWVT IIAQVLMNVVSMQADCRMN LLEIFLRWLMRIIFHVRLLPAVS TPTNCLNQLLFFLTPVNYLPG QSGTTVPLVSSV

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13448	43816	A	13528	273	688	SHPPFFSTDWSTDGTVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNMGVSMPADCRMN LLEIFLRWLMRKIFTTGLRSFGL VKQKKSPIRMPCVYTNPVCVSIV SRMGQASSL
13449	43817	B	13529	1	1053	
13450	43818	B	13530	1	1869	
13451	43819	A	13531	120	430	EDLSDTGVRSKSIWCHRNCRW/ RVAVVKLLHLPKVII VFWLASW MMSRWLHYPDWVTIIAQQVL MNVVSVMQADCRMNLEIFLR WLMRKIFHSSLEDPRNWL
13452	43820	B	13532	148	334	
13453	43821	A	13533	2	147	TSMDBKLGQALKKKI*DL*KK* LKNIPVDKWITPREVFSGIVCK QNI
13454	43822	A	13534	151	325	KAICHNTFSKPSMDKGL/LRRS KKEGFKTYKKNIYKNIPVDKWI TPREVFSGIVCKQNI
13455	43823	A	13535	283	406	HRTKISIVPEGIFKSFSPLAGIM TEQYFL*TLHRLRLIM
13456	43824	B	13536	1	1902	
13457	43825	A	13537	508	1041	LWREASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPW/C YQTIWHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIDWIIERYQLPQSYQRPDPF RRRFLQVCVNEINSRTPMRLSYI EKKKGQRQITHIVFSFRDITSMIT
13458	43826	A	13538	1	1422	
13459	43827	B	13539	1	1002	

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13460	43828	A	13540	1	160	MVLIVAATV VVVVVVGLCWM AKSECRSAMRLSSLQVRIFTYLI GREAAFADNLKWMACANKES ALLDRFIFLILLCKEPWECHCL PLFKVAMP SKCDIPVICA HINIG FTLRQLRGFGPCNIGSFEAKDS KNPQVRVISQKHKALRCIWFIT CSICNPEFTEGALQGNKQRKRQ CLQWFRKALESNEPGFEFIQD KLLTQSLCFFPYTFLWLTGPHPS GSSYTDPCSSKADVTPSSAVQ EHSSALELKTIVSPITRQQHGF FTQISTLADVQENVMEYLHVLS RPKVIDQEHDVVWTEAYIDSTV CRVKRRQLLLQVPLTRKQQF LPAPYVDLDSARTRTNKQQQN PIIYTGSKQGSVILFHYGESWN LLRADQRLIFAKSWPRASRYQQ GHQDLFILRSDLPSQVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYVTK VFALDVAARHRVQFAMPESDA VAMLKQL*QPQWWWSW*D CAGWRKVNAAPCVCLPFRFA SSHTSLDERLRLQTI
13461	43829	A	13541	48	668	
13462	43830	A	13542	1	1278	
13463	43831	A	13543	100	157	
13464	43832	A	13544	1	1122	
13465	43833	B	13545	1	1131	
13466	43834	A	13546	273	812	SHPFSTDWSTDTGVRKSIWC HRNCRWESPS*SC/WHLPKVILV FWLASWMMSRWLNYPDWVTII AQQLVMNVVSMQADC/KRIC WKYFCAG*CGKIFTYQ**TWN NTETSM SQPKCKMKRI/YSREE LAV*KMDHSDLSLW*KLEPL TCRSTSHFRQKLAQGFVPSTGT PGFIYS AK
13467	43835	B	13547	1	987	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13468	43836	A	13548	246	2065	LVGWLGDGWLGDGWLIVLALPFM MIPWHSSIQPFTHPFNWNFG*M PELCPQINGMDSWLAGWM/CWL DGWLGDG*MAKLKRPVL*PD KEGNEIWDVMTVKPSGWTVR TFDKPRKRFI AFFIAGILFRAIKN HFLPRETLQCLPYILTGFRGQS EYFSIFSNDMLADTVMFLIVL PFMMIPWHSSIQPFTHPFNWNF G
13469	43837	A	13549	2	118	
13470	43838	A	13550	397	729	THGIRIGDFFCFTKRKLKRPVL* PDKEGNEIWDVMTVKPSGWT VRTFDKPRKRFI AFFIAGILFRAI KNHFLPRETLQCLPYILTGFRG QSEYFSIFSNDMLADTVMFL
13471	43839	A	13551	147	417	SSSWGRSSPQLVCGIFQTAGPQS LCKWNQ*VLAQTNKKTAGTSA DLVVPV*QL*RKAVVLPNTAP WRFWRTRQEWFSRGRSGYQS QET
13472	43840	A	13552	1	2418	
13473	43841	B	13553	1	1848	
13474	43842	A	13554	188	490	EWRNVCGVTGTEKVTPSAAAA ATASPIQVLTIVSVTSQIRAFSV LPVRLRRSMLSRLNTCVNRF CNPICKGMRYGLICPL*SLLDGL CARLINQKGDS
13475	43843	A	13555	83	440	SLLFKCSGVIVLRRPLGYRQVM NVTTRCCLLRTHWMISLLFY*L VNRHRSVEEYLVSYTLPMGV AVVKLLHLPKNFVSLITPRGRL EKERAF LFQHMRSISTGLKIFV MHTSCPMVVC

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13476	43844	A	13556	1337	2583	QQR*MCQNLMT*HQNRSGR SQNDF*RRRNISERSAVYR*R QLYIRRPQYAEPSVHVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFRKESQKLQ SAKKRDAELANGALGIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYTK VFALDVAARJIRIKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAKGVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLIPFFIGLQNR TQFRLSEKTIINPYAMRVTNP CVSIVCVNEINSRTPMRLSYIEK KKGRQTTHIVFSFRDITSMITG
13477	43845	B	13557	1	696	
13478	43846	A	13558	326	1577	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQR*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHRRH
13479	43847	B	13559	1	3822	
13480	43848	A	13560	848	1476	VNVTSFGSRPICSTSPVLSGL* GPVKEFDT*PSM*ISFELIPSVIF EPRESVNKYHLPILKTFARSISS VTVEVISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFYEVFMAFVFNVV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
13481	43849	A	13561	1	2196	
13482	43850	A	13562	326	3746	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRS*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHRRH*SCRYPS*ARCQ*LTG QIVHRGEKKEQLI
13483	43851	A	13563	3802	4075	IRCFYSPAPGYFPFRFRAVHKL NGDSLRFHMTSVYALQEA VRHTLVTLRQLVTLDPVDFQ RDDA*AIRAYDGTGIRINAWH TDW
13484	43852	A	13564	1708	3198	
13485	43853	A	13565	1	1401	
13486	43854	A	13566	1214	1357	NKINMFIAALFTIAKT*WNQPK\ CPTMIDWIKRGSSRVASSSSPT RTR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
13487	43855	A	13567	3363	3852	SHPFSTDWSSDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMRSRWLHYPDWVT IIAQQVLMNVVSMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLFFLTPVNYLPG QGFAGFRNPPSNRIFACWGKPA WTACCNLSLRARR
13488	43856	B	13568	350	742	
13489	43857	A	13569	248	599	HRDSYKRMAYGLVISVVSLSR KLKRPVL*PDKEGNEIWVDMY TVKPSGWTVRTFDKPRKRFI FIAGILFRAIKNHFLPRETLQCLP YILTGFRRGQSEYFISFNMDLA DTVMFL
13490	43858	B	13570	1	2148	
13491	43859	A	13571	3064	5069	RSDPDENCC* TGH*STLFNWC WRNALSIWEPVCNEIFYRLIKPR WEIRWGKRAPVIPKHTLNTQPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSLTGGQTP AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGELDDQMAA LSRLGNDYRPTSA YERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSPHRQ APCMKSNNALIVILGTVTLDAV GIGLVMPDLALKGLRVLLVEG NDPQGTASMYHGWWPDLHIHA EDTLLPFYLGEKDDVTYAIKPT CWPGLDIIIPSCALHRIETELMG KFDEGKLPTDPLMLRLAIETV AHDYDVVIDSAPNLGIGTINVV CAAAHALIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPPD RILLTKYSNSNGSQSPWIEQIS DAWGSMLKNVHAIVTGDVAV GMDDIPQEARQYRHNQAYAYS IQGDGAEDDDERIVRFHTRVT DSDTLASDAARLTCRHGLGNQ RNGGVLIEDKFECFFSLTA VFA TRAYYAVYHLTGARHSDIVVA HGYAGCNVRFVALLGTNTTLE TYLSNQGSNGFSLHFGEVDVGQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
13492	43860	A	13572	1408	5578	CSHLIIQLANQNTHITFGKCSF TTATPIGNFYDTRYSSSTERRCLL TSQ*KRRDEIIQCVLKQLRAR SLPDPTRKVFSTLSRSTFRVNF TSRPHTGKVFVAFREPFLPPHL RKPDITDTGYLYKRMAYGSVIS/ ICFTKPKLRKPVL*PDKEGNEIW VDMYTVKPSGWTVRTFDKPRK RFIAFFIAGILFRAIKNHFLPRET LQCLPYILTGFRGQSEYFSIFS NMDLADTVMFL
13493	43861	A	13573	2678	2884	SAPLQRNTARRFLFLKACSNR FCYRWRHMTAIPSYNRSKRLREI KGGLYHMGIFRRFLASKETPTF CY
13494	43862	B	13574	1	7903	
13495	43863	A	13575	1	880	
13496	43864	A	13576	1	996	
13497	43865	A	13577	763	778	NRCEPPV*GTRFSQQLLLAKA TLLIEELYALTVHSWRPKW
13498	43866	A	13578	2	254	
13499	43867	A	13579	1	2358	
13500	43868	A	13580	206	382	
13501	43869	C	13581	1	1137	
13502	43870	A	13582	79	906	
13503	43871	A	13583	2	383	SPPEVVRLLGYHPPRHGHQ*HLF ASCRKGDVGRVRP*TRPDPGSD LLPAQVPAGAARRGGTMPACV GTRSWYSTFWMEPAARPTPS MVSAASMGGH*VTPSAGLYAITS RSRLPAGGGITMTTSCSGF
13504	43872	A	13584	1	1092	
13505	43873	A	13585	173	262	
13506	43874	A	13586	898	1391	QLGILRVNLLGIDLRVTGHQAA PPLHLLDLLQMH/SSPPCRPQ*A TSPPPSLRCRAPHR*SLAAP*A PPPRPFLSAGSPHRKGGPGPAPT GSWSSGNQAGLPCCLGWASVF LCPSHLPPHLPQSSASLAFHRV KHLHLHNSVIDKMKYQLKFLC LLGEYLSV
13507	43875	A	13587	1	960	
13508	43876	A	13588	1318	1369	RDFHPK*HTGIQYIWQQLEINQ CDTSLSMVLPR*RDHFHPKSHLL PGAAQIQ
13509	43877	A	13589	212	385	
13510	43878	A	13590	377	505	
13511	43879	A	13591	69	193	CSLRSLAQMLPFYPRRSCLSCS L**PHCCLWLAALRSESK
13512	43880	A	13592	1	230	
13513	43881	A	13593	2	341	

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13514	43882	A	13594	1	2421	
13515	43883	A	13595	1	623	
13516	43884	A	13596	1	906	
13517	43885	A	13597	1	568	
13518	43886	A	13598	107	199	
13519	43887	A	13599	42	328	GGASGVCSF*CSE/LSSFWWVR GLAGSGVKLQTFATQEPSWLH PVPDPVGLQVELPASPAPCART PQPLGGRWDSAPWSRGRSSG AHGIDVALLP
13520	43888	A	13600	5	124	IWLWFFVSLT*RSRGSQ*VLQ LIKAPHVDLLVVTFC
13521	43889	A	13601	827	973	HHQSALCI*LKFYTSLTHPVISLV VETLVVW*YLYKM*KKLWSWI RGRG
13522	43890	A	13602	2	503	
13523	43891	A	13603	56	792	
13524	43892	A	13604	1	411	
13525	43893	A	13605	1	1554	
13526	43894	A	13606	1	363	
13527	43895	A	13607	1	966	
13528	43896	A	13608	932	1189	
13529	43897	A	13609	146	323	
13530	43898	A	13610	1	1827	
13531	43899	A	13611	2	412	
13532	43900	A	13612	1	2238	
13533	43901	A	13613	2	411	GATDCVCYYTVGFNDTKTSAL HMYVGDGLAMDVSSVHIINSTL LRYSVTLGFGYGDIIKDSDK KRRRLGLARYDFLCKTFFSHH* YEGTVTFLPAQHTVGSPRDRKP CRAGCFVCRQSKQQLLEEQKT ALYGLEL
13534	43902	A	13614	3	2185	
13535	43903	A	13615	206	1568	
13536	43904	A	13616	165	417	TWDYIRPNE*YM*MAKKKMP MD/VWCNGKNWRPAG.EFVDD GVTETHFSIGNHDCYKAVSSGK RKEGIIHTLVDNREIPEIAS
13537	43905	A	13617	463	837	
13538	43906	A	13618	1	765	
13539	43907	A	13619	3	510	AGVHKIEFEHGTSGKRVVVV DGKEEIRKEWMFKLVGKETFY VGAATKATINIDAIISGFAYEY TLEINGSLKKYMEDRSKTTNT WVLHMDGENFRJVLKEDAMD VWCHGKGIKRRPAGFVDDGTE TPLQYPGPMTCYIKAVSSGKR KEGIIHTLVDNREIPEIAS
13540	43908	A	13620	342	585	
13541	43909	A	13621	1	1119	

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13542	43910	B	13622	48	1104	
13543	43911	A	13623	656	916	GWRKYLQGAADMGIAEGGGS VWSSWASSLSISVPVR*LCES TSQ RSAPGWPLTGGSCSEVALWL CVNDFEFQMRLMPSRDSEPA
13544	43912	A	13624	179	682	
13545	43913	A	13625	1	7511	
13546	43914	A	13626	56	8669	
13547	43915	A	13627	42	8716	
13548	43916	A	13628	1	2457	
13549	43917	A	13629	3	571	
13550	43918	A	13630	1	867	
13551	43919	A	13631	1	2238	
13552	43920	A	13632	171	396	
13553	43921	A	13633	1	3940	
13554	43922	A	13634	554	619	
13555	43923	A	13635	1	1359	
13556	43924	C	13636	208	359	
13557	43925	A	13637	2	513	PSHDHSLKGLTRASGKVLHGEH AAVHGKVALAVSLNLRITFLRL QPHSNGKGDLSLPNIGIKRAW D VARLQSLDTSFL/RWTKEDLELI NKWAFQGERMIHGNPSGVDNA VSTWGGALRYHQKISSLRSP ALQILLTSTRG/PRNIRALVGGG RNRL/LEVPMGGPILLSW
13558	43926	A	13638	3	1331	RVDDFVGELLRLRRGGADVE AAAAAGFPAGMLSQVLLVSAP GKVLHGEHAVVHGKVALAVS LNLRTFLRLQPHSNGKVDLNL P NIGIMRAWDVARLHSLDTSFLG ECKEEKPEQGDVTTPTSEQVEK LKEVAGLPDDCAVTERLAVLA FLYLILSICKQALPSL/DIVV WSELPPGAGLGGSSAAYSVC LA AALLTVCEEIPNPKDGD/CVN R/WTKED/LEL/NK/WAF/QGER MIHGNP/SGV/DNAVQHLGEGA LRLPSRGRFSFL*RGSPVFQI/LG LTNTKVP/SAITRALVAGVRNRL LKFP/IVAPLLTSIDALS/ECERV LGEMGEAPAEQYL/VLEELIDM NQHHNLALGVGHASLDQLCQV TRARGLHSLKTGAGGGGCGITL LKPGLEQPEVEATKQALTSCGF DCL/ETSIGAPGVSIHSATSLDSR
13559	43927	A	13639	1	950	
13560	43928	A	13640	1	1653	
13561	43929	A	13641	1	2601	
13562	43930	A	13642	2	513	
13563	43931	A	13643	47	367	

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13564	43932	A	13644	1	633	
13565	43933	B	13645	1	1110	
13566	43934	A	13646	172	1095	
13567	43935	A	13647	1	855	
13568	43936	A	13648	3	440	
13569	43937	A	13649	2	230	
13570	43938	A	13650	2	606	AEFDLCCSPCRRRLLGREEAGE EPTSPVTQYLQPRSPPECKMFA CAKLAICTP*SLJRAGSRVAYRPI SASVLSRPEASRTGEGSTVFNG A\QNGVVSQ/LIPKGSFKTSAISKK TLDTA\AKFIGAGAGNS*GVG WFLVAGIG\TVFWASLIHWVM ARKPFRWKQQLFSYA\ILGICL VLKAMGSPFVLMVAFILFAHV TEITA
13571	43939	A	13651	200	2320	
13572	43940	A	13652	224	640	
13573	43941	A	13653	1	357	
13574	43942	A	13654	43	183	
13575	43943	A	13655	3	478	SSAGREPDPSDLPRRLCFTHRLP AARRVWVQLCVHASPEPGGQGV CPGRSERMVRVFIASSGFVAI KKKQDQVVRFLANKIEFEEVD ITMSEEQRWMYKNVPPDKKP TQGNPLPPQIFNGDRYCGDYD RLFESKESNTVFSFLGLKPLAS KAEP
13576	43944	A	13656	2	428	CRDGKDVVSLVRATVWALSKR KLQPTR/ALTPPSAVNLIKQF LKDKPELVDVKVGVRTGCNG LSYTVETKTKGNSDEVIQDEA RVFIEKKAQLTPLGTEMDYVED KLSSE/FMFNNPT*TCGCGAPGK LVETLGLTEIM
13577	43945	A	13657	1	1377	
13578	43946	A	13658	1	1215	
13579	43947	A	13659	1	452	REAEAADLRSEAPGRDGEDV GFLSSGQLSLGCKRKLQPTR ALTLPASAVNLIKQLLKE*P*AC R\LKVGVRTRGCNGLSYTLEYT KTKGDSDEVIQDGVVRVIEK\K AQLTLL*TEMDYVEDKLSKGV GVH\SPNIKGTCCGESFNI
13580	43948	A	13660	3	763	
13581	43949	A	13661	1	306	
13582	43950	A	13662	738	1022	GQHHPETKAWQRHNKKREF*T NILDEH*CKNP*NTGKPNPAT HQKAYPP*SSGLHPWDARLVQ HTKINKCNPAYKQNRQKPHD YLNRCRKGL

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13583	43951	A	13663	2	516	QKIDLPYQGEPEISIQKCQEA VRQVQGPVLVEDTCLCFNALG GLPGPYIKWFLKLPKPEGLHQ FLAGVEGKSAAYALCTFALSTG DPSQPVRLFRGRTSGRIVAPRA CQDFGWD/PCFQPDGYEQTYAE MPKAEKNAVSHRFRA/LELQ EYFGKFGQLDFCKLEAGPFR
13584	43952	A	13664	7	227	
13585	43953	A	13665	1	415	
13586	43954	A	13666	234	510	
13587	43955	A	13667	2	402	
13588	43956	B	13668	530	1544	
13589	43957	A	13669	1	603	
13590	43958	B	13670	1	1527	
13591	43959	A	13671	1	1179	
13592	43960	A	13672	2	413	
13593	43961	A	13673	100	374	KHISPAKALELPFERNLI/PLQ LLKVRILKEGEM/LD/*HWFL** GMGTQVKGMPHKCYIIGKTGR VYNTQHAVGIVVNVKQV*VV
13594	43962	A	13674	1	1035	
13595	43963	A	13675	2	564	GPFGRRNRHLPVIRQNDGPQRGK RRGTPKYVF*/RPFRR/HGGGPL GPPYMRIVRKGDIVD/LKGMG/ TVQNGMPHKCYHGGKTGRVYN VTQHAVGIVVNVK/QVKGKILA KIRINVRIE/H/KHSKSPR*ASLK/ RVLEKNDQEKERSPKKGTWG SNLKRHPAPPQKKHTL*RTNGK EPELLEPIPYEFHGHN
13596	43964	B	13676	68	391	
13597	43965	A	13677	1	404	PTRTWTRGRIPLSAPPSSRGAR GTMA DPRVRQIKIKTG/VKRL VKEGVLYEKEPKQ/QEEKIEKM RAEDGENYDIKKQAEIL/QESR MMIPDCQRRLEAA YLDLQRILE NEKDL/EAE EYK EARLVLDSV KLEA
13598	43966	A	13678	1	436	LLACRSMDCYLAIVHATRTLT QQRHLVKFICLGLRNLFLLLSL RILLFRRTFYPSNVSPVCYEDM GNNTANWMLRLILPQSFQIV PL/LIMLFCYRFTLH/LFKAHMG QKHWTMWVIFADVLI/LLCWL PYNLVLADTIMGT
13599	43967	A	13679	1	705	
13600	43968	A	13680	292	1489	
13601	43969	A	13681	434	1205	
13602	43970	A	13682	1	390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13603	43971	A	13683	21	479	TYPEAWKLYYRSR*SRDLRKY HAHSVSP*QDQRYTS*KILKCD EHIKLGLGSCITDPGNRETSNGT MHTVFHRDKTKDTHPESCCSSE KGGQPLPWFEHRKNVPQFAEP TETLFGPDSGKGAKSLVELLDE SECTSDDEIFISQDEIQSFMANN QSFYSNREQYRQHLKEKFNKY CRLNDHKRPICSGWVDNGWEA
13604	43972	B	13684	32	438	
13605	43973	A	13685	533	1226	
13606	43974	A	13686	1	1566	
13607	43975	A	13687	215	453	
13608	43976	A	13688	1	553	RRPARAAVIKQPPAPGASQHAA TPTQTPLCTPARPLPPMAHVQQ LEGRWRLVDS\KGF**NTMKE\I GVTIALRKMGRNAQAQICIT\TS DG*NPSPKTESTLKT\TQFSC/T LWGEKFEETTA\DGQKKLTNCL STFPDGA\ALVQHQEWDERKS TVTKKN*KDGEISWLECVMMN\I VTCTPDSMKK
13609	43977	C	13689	11	106	
13610	43978	A	13690	3	155	LCELQKAIDLFTDAIKLNRLAI LYAKRASVFVKLQKPNAAIRD CDRAIEINPDSAQPYKWRGKAH R*ILAWPFCMPRGVSSSNYRS QMLPSETVTEPLK
13611	43979	A	13691	1	1732	
13612	43980	B	13692	95	1715	
13613	43981	A	13693	1	446	
13614	43982	A	13694	1	786	
13615	43983	A	13695	88	828	

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13616	43984	A	13696	157	1515	RREKMAELKYISGFGNECSSED PRCPGSLPEGQNNPQVCPYNLY AEQLSGSAFTCPRSTNKRSLWLY RILPSVSHKPFESIDEGHVTHNW DEVDPDPNQLRWKPFEPKASQ KKVDFVSGHLTLCCGAGDIKSN NGLAIHIFLCNTSMENRCFYNS DGDFLIVPQKGNLLIYTEFGKM LVQPNEICVIQGMRFSDIVFEE TRGYILEVYGVHFFELPDLP ANGLANPRDLFIAPWYEDRQV PGGYTVINKYQKGLFAAKQDV SPFNVVVAWHGNYTPYKYNLKA NFMVINSVAFDHADPSFTVLT AKSVRPGVAIADFVIFPRWGV ADKTSGPPYYHRNCMKRFME LIRGQFEQKQGWFLPGGRG/SL HSTMTPHGPDADCFEKASKVK LALKRIADGTMA/FMF*SSFNLA GPKWGLQAPRVLDKNYPKCW EPLKSPFVTPNSRNPAPEN
13617	43985	A	13697	1	156	
13618	43986	A	13698	8	306	
13619	43987	C	13699	1	1143	
13620	43988	A	13700	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPFEDQEGGQRLRSSHIR LGQFLLIEDCKTPSPSLGADAI AKQRKTSVSAASVSATIPIRR VQGPTVVGSWARGVSAASGP RGTGPKGKARSEKGCSSLSHGPQ TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSH LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAIYMNMGKGL PIWCHLLEEGIYLEVWALEGQF GRAKNACPQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGWQKP NGQWSLVQDLRLISEAVIPLY VVPNPYTLSSQIPEAEWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPGQFR DSPHLFGQALAQDLGHFSPGT LVLYYVDDLLLTSSSEASCQQA TLDLLNFLANQGQYKASRSKAQ LCLQQVKYLGILARGTRTLGK ERIQPILAYPHPKTLKQLWGLF QIT/GFCQLWIPR*SKI
13621	43989	A	13701	188	688	

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13622	43990	A	13702	636	2628	SNDRTEDDCGKHPPMSSPPTEP WVCLIEGQEIDFLDTGTTFVS LIPCLGRLSSRSVTIQGILGQPV RYFSLHLLSCNWETLLFSHAFLV MPESPPTLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDP SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPI LG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLISQVPEEAEW FTVLDLKD
13623	43991	B	13703	302	619	
13624	43992	A	13704	1	5172	
13625	43993	A	13705	1	2091	
13626	43994	A	13706	1	1754	GPRGTGPGKARSEKGCSSLHG PQTNKPLVVQKGQKMEQANHP VGLVISVYKDIKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIYMNMG N KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDP TTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPI LGVQ KPNGQWSLVQDLRLISEA VIPL YPVVPNPYTLLSQIPEEAE WFP VLDLKDFAFFIPLHYD SHDSQF LFAFEDPTDHTS QLIWTVL PQG FRDSPHLFGQALADLGH FSSP GTLVLQYVDDLLAT SSEASQ QATLDLLNFLANQGYK ASRSK AQLCLQVKYLGIL LARGTRTL GKERIQPILAYPHPK TLKQLWG FLEITGFC*LWIPGY SKIARPLYT LIKETQRANTHL VEWESEETA FKTLKQALVQAPGL SLPTGQNF SLYVTERAGIALGV LTQTRGTT PQPVAHL SKETD VVAKWPHC LRVVA AVLVSEAIKIQGKD LIVWTT HEVNGILG/AGKSL WL SDKRLFRYQALC LEGLVLIQRT SCGSHLAVTRLWALYF
13627	43995	A	13707	2	887	

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13628	43996	A	13708	3	1750	GWAVPRPGPRGLTVATEAAAA AAAAAAAIISSRTRAPQAEGR NRRLEKMADDIDIEAMLEAPY KKDENKLSSANGHEERSKKRK KSKSRSSHERKRSKSKERKRS RDRERKKSKSRERKRSRSEKRR RSRSRSDRRFRGRYRSPYSGP KFNSAIRGKIGLPHSIKLSRRRS RSKSPFRKDKSPVREPIDNLTP ERDARTVFCMQLAARIRPRDLE EFFSTVGKVRDVRMISDRNSRR SGIAYVEFVDVSSVPLAIGLTG QRLGVPIIVQASAEKINRAA AMANNLQKGSAGPMRLYVGSS HFNITEDMLRGIFEPFGRIESQL MMDSETGRSKGYGITFSDSEC AKKALEQLNGFELAGRPMKVG HVTERTDASSASSFLDSELER TGIDLTGTGRLQLMARLAEG TGLQIPPAQQAQMSGLAF GAVGRNLCYRFQKQDFSHQT ETSALSAASVQPLATQCFQLS NMFNPQTEKEVGWDTEIKDDV IEECNKHGGVHIHYVDKNSAQG NVYVVKCPSIAEIAAVNALHGR WFAGKMITAAYVPLPTYHNL PDSMTATQLLVPSRR
13629	43997	A	13709	141	343	LHEGLLP*RGHALLSGALHG*C VGSLFSTPRCLTSSACGYPS CTPGSCTAWCPSASRRRLSCWT
13630	43998	A	13710	5	426	
13631	43999	A	13711	1	1188	
13632	44000	A	13712	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEDP NCHEQHLSENTAHLTGDTQEA VDGRRKPEESRTTSHICRCS
13633	44001	A	13713	1	700	
13634	44002	A	13714	3	483	
13635	44003	A	13715	2	361	RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNLKIIISNA SCTTNCLA/PPASTGAAKAVGK VPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13636	44004	A	13716	2	249	SADAPMFDMGVNHEKYDNL NII/SVMKAGPVEKRPAPWH PMDTLP*LAPRSLFLCSNASCTTN CL EPLAKVIHDFNGIVEGLMV

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13637	44005	A	13717	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKGVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQERYPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPADAPM FVMGVNHEKYDNSLKIIISNA/S CTTNCLT/PLAKVIHDNFGIVEG LMTTVHAITATQKTVDPGSGKL WRDGRGALQNIIPASTGAACA VGKVIPELNGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVKQA/SEGPKLGILGYTEH QVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13638	44006	A	13718	3	483	
13639	44007	A	13719	2	361	RRFRAGAGYVVESTGVFTTME KAGAHQGGAKRVIISAPADT PMFVMGVNHEKYDNSLKIIISNA SCTTNCLA/PASTGAACAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13640	44008	A	13720	2	249	SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRP/WHPM D TLP*/LAPRSLFCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
13641	44009	A	13721	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKGVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQERYPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPADAPM FVMGVNHEKYDNSLKIIISNA/S CTTNCLT/PLAKVIHDNFGIVEG LMTTVHAITATQKTVDPGSGKL WRDGRGALQNIIPASTGAACA VGKVIPELNGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVKQA/SEGPKLGILGYTEH QVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13642	44010	C	13722	40	243	
13643	44011	A	13723	2	2972	
13644	44012	A	13724	1	602	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13645	44013	A	13725	1	325	MGRNQSRKAENTKNESASSPP KDRNSSPVREQSWTENEFDEL EVGFRKLVTITNFSELKEHVLTD HKEAKNLEKS\LEVVAAREISQE KEIKVFN*EKRSKNCPLQMT
13646	44014	A	13726	1	981	
13647	44015	A	13727	1	739	MGRNQSRKAENSKNQSTSSPPK DCSSSPAREQNWTKNEFDELTE VGFRRLIANFSKLKECVLTHR KEAKNLEKSDRENGTKLENTL QDIIQENFPNLRQANIQIEIQ RIPQRYSLRRATPRHII\VRFTKV EMKEKMSRAAREKGRVTHKG KPIRLTADLSAENLQARREWGP VFNLK\NFQPRIPYPAKLSFISG GEIKSFDTKQMLRDFFTTRPAL QELLKEALNMERNNQYKPLQK HAKW
13648	44016	A	13728	1	1277	MKEQNGGGGREEDHKDKGIRQ LPSSLPSAGEAKSDKPEHHNRY RKEIASFEDEKRAMGVAKMAE QEQLQSAAPSMTNAEVGTAHG GRAEAGRGVDSPGKRKVLGDF PFLAKGSRDRLPGKAGHSLPKY YAFTKVLATGRQERNINISKK VIYTKTTSTGHQHPKIDKTT KMGRNQSRKAENSKNESTSSPP KGHSSSPATEQSGTENDFDEL EVGFRRSVTTNFYELKEDVQTH RKEAKNLEKRLDKWLTRINSV EKTLSDMELKTMARELRDTC SSFKSFRNQVEERVSVIEDPIYE LSREDKVRDKKVRNKQSLQEI WDYVVRPNLRVIGVPESDGEN GTKLENMLQDIIQENFPNLRQ ANIQIEIQRTQRYSSRRATPR HII\VRFTK\VEMKQKVLRAAREK GPVTHKGNSGSL
13649	44017	A	13729	1	1584	
13650	44018	A	13730	493	575	SHPMPNPANTRSQRNPTKKKQ KKNV\CDNIRELEQQMEDAYR GTRKRMPLSSSSMRSDGFDEE SQRYYWRPKNEISGLEDLFLK AKSWNRKFYDYANMPDRWG\ QVAIKSYTLKNLQTVVISIKLP TGRKHLPR*SHPMPNPANTRSQ RNPTKKKQKKNVCG
13651	44019	A	13731	1	655	
13652	44020	A	13732	2	1664	
13653	44021	A	13733	1	2364	
13654	44022	A	13734	1	224	

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13655	44023	A	13735	1033	7511	
13656	44024	A	13736	56	8669	
13657	44025	A	13737	42	8716	
13658	44026	A	13738	1	5046	
13659	44027	A	13739	1	2298	
13660	44028	A	13740	1	2362	
13661	44029	A	13741	1	2046	
13662	44030	A	13742	1	1503	
13663	44031	A	13743	1	813	
13664	44032	A	13744	185	735	
13665	44033	B	13745	317	910	
13666	44034	A	13746	1	867	
13667	44035	B	13747	1	2325	
13668	44036	A	13748	1	430	
13669	44037	A	13749	1	867	
13670	44038	A	13750	35	518	CLSRASPVLASMSGRGKTG GKARAKAKSRSSRAGLQFPVG RVHRLLRKGHYAERVGAGAPV VLAAWLEVAQPLRVLELAGN AA/RSNKKTRIIPRHLQLAIRND EEL*KLPGLP*RIAQGSRLVLPNI QA/VLLPKKTSATVGP/PAKPSG GKKATQASQEY
13671	44039	A	13751	1	937	
13672	44040	A	13752	1	1096	
13673	44041	A	13753	85	1512	
13674	44042	A	13754	3	2377	
13675	44043	A	13755	1	1134	
13676	44044	A	13756	49	408	
13677	44045	A	13757	47	2603	
13678	44046	A	13758	1	378	
13679	44047	A	13759	1	696	
13680	44048	A	13760	3	401	
13681	44049	A	13761	882	1106	KLHPYTTRQYCHFRI*TDVMAK RSRNAVKGSLVWCAISDFA AGFTPDGCTRAFTFTGGWRK RDCRGAVAGG
13682	44050	A	13762	688	1100	
13683	44051	A	13763	476	552	
13684	44052	B	13764	178	1107	
13685	44053	A	13765	1	198	
13686	44054	B	13766	94	625	
13687	44055	A	13767	1	732	
13688	44056	A	13768	1	4443	
13689	44057	A	13769	216	575	PGAGDRYVGKPVSAVGTAVSC GVWSSMPDATLIASYQAYTSH VGRIRRSRRIR/TNTARADYPAL TALPFNNFRTHNRFGNAAVSL ASIGIGSSLICARISAHSGAEH KPPEPKAANIK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13690	44058	A	13770	1018	1489	KLPGQRRFVQTPSHVLHTLSYPTAPAQSSYPAPLSPSQDRAPTLAHQTT*FSASYTANAQWQRVAADHLKSVRETYAHVRQFSPALGNAPPDQLPLS*ASCVPKSGARYSSVIRQNRDRFFRATDHMYVTVPTRPKMWNPNVTQMNPSFRA DTCE
13691	44059	A	13771	1013	1755	GSPGLRPGGAAGKALAPSGCTGNSHRAMP*PGAQAQTRPEKW A*QRP/HVSTGARGARVRALAA VAAAEAQRAAGAAVRAAALHTRAAVSAGAAARAVVQVVLAA RTREAGAAAAAQGVAQVQAES AIAAWLQAAPVHPLLTVGALE TGWAVADVGRVRCPTDPTQA AVEAGSICTCHPAHLTPQPVEPTRAGAFKGPGLTTAASIGTRVPVTGPRPRDKASGGSRGRAPGA EAAAGGDRDRAEGSSPAL
13692	44060	A	13772	1	1236	
13693	44061	A	13773	1	456	
13694	44062	A	13774	1	219	
13695	44063	A	13775	1707	1853	
13696	44064	A	13776	1	615	QLATFFFGGLPGGSAPWDPPGEACLWVLVRLPGRTVWVIQFVQLRSFFAPPFANHGRASSGRVS VHYGIAQTAEWAAEICGVGAR KIRELAAIFHQNTIMHFANGG/NPTRRSVAVLSSMQGSLPGGCDAVDIHPVARIVEALENPGGAYQHNGMNRHFDPDIRFIWWAGGANFTHHQDTNRLIRA WQNDYSYFRKGRIKAKMGPKLF
13697	44065	A	13777	407	661	ANWIKWRWIIRAMIHSSSSMWQTANSLASFISAPVTSSACRSTLPATRYWCI*WRSSAIWKWVILSGPVATRICTATIWIQLICN
13698	44066	A	13778	1	2448	
13699	44067	A	13779	3	1612	
13700	44068	A	13780	1	1626	
13701	44069	A	13781	3	118	
13702	44070	A	13782	1175	1396	
13703	44071	A	13783	197	933	
13704	44072	A	13784	2	64	IILLNSAPAWM*TFKLPGVDVNYMLHTQNK
13705	44073	A	13785	1	855	
13706	44074	B	13786	1	1605	
13707	44075	A	13787	1	588	
13708	44076	A	13788	1	2769	
13709	44077	A	13789	813	1341	

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13710	44078	B	13790	1	999	
13711	44079	A	13791	1	281	
13712	44080	A	13792	1	1332	
13713	44081	A	13793	1	1384	MPITLRRSVEKEQLIEANTIMPF GKYKGRRLIDLPEEYLLWFARK DEFFPAEARYTHIDLHVPAPLLV MFTLDTRQSACDRNP.H.PIHVC SSWTSKCAPRLWTRALLPRTR TPPYATGTTIGSRASWFVTFPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLHKM VEVNACLKQLDNKDADIADYEHN QLMRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSVVVEETR EAVDTSQPVAT
13714	44082	A	13794	1	2004	MTQQITLIKDKILSDNYFTLHNI TYDLTRKDGVEVIRHKREVVYDR GNGATILLYNTKKKTIVVLIRQF RVATWVNGNESGQLIESCAGL LDNDEPEVCIRKEAIEETGYEV GEVRKLFELYMSPGGVTLEIHF FIAEYSDNQRANARGGVEDEDI EVLELVQCGGQIGVPTVLAVF ATGIGFLAMSVTKPRINAQPPY MPWRNL.AQL.VEHINRTRIHRNL QFTDAFKRRLIDNICRKNNIIGT HTGQSKFSGQTQIFGEIPQVVP ASELAAMKQIKELQRLLGKK TMENELLKEAVEYGRAKKWIA HAPLLPGDGERTDDWMDGRRS RHTDDTDVLLRIHHVIGELPTY GYRRVWALLRRQAELDGMPIA NAKRKYRIMRQNALLERKPA VPPSKRAHTGRVAVKESNQRW CSDGFECFCDNGERLVRTFALD CCDRLSSRGRNAAAKRQRDDP LRWKFRLPSSGQTKLLMPLDQ APARFAPVFTCTLTILCGTHV VYTIPIHYDVAIKNNIRPERPM AASSIGAQMGHASPVSVAVVS VAMLGNVTFDGRHLEFLDLLAI TIPSTLIGILAIGIFSWFRGKDLD KDEEFQKFISVPENREYVYGD ATLLDKKLPKSNWLA MWIFLG AIAVIALLGADSDLRSSF/GGKP

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13715	44083	A	13795	3	918	DKTRKRRIRQ*IPNATSFYQNS PGLSE*LAAGTWTFAGNAPASS CGFRDRYLIVCSHQTPHVPQGI TVAAPDARAQAIRIVRQLQRF FHRFEGGHRQHRANKLLLEHP HIVLTQKNRRFEADALQPDPA WQQGTLSNGLQWQVLTTPQR SDRVEIRLLVNTGSLAESTQQS GYSHAIPRIALTQSGGLDAAQA RSLWQQGIDPKRPMPPVIVSYD TTLFNLISLPNNRNDLKEALSY LANATGKLTITPETINHALQSH DMVATLVFRYLKKGWWRYL KGSTLLSHDPAHPLKQVVEAK
13716	44084	A	13796	1	1368	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAVYGIWMA ETMFAPACYGYILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVCVFGWIFAAIKRDA AAGRAKENVIFHHFPQSVKAD IATNPFKRPGGAFIRITQFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNPLDSSVLSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTGAIPFAAADPLR/PSFGG KPLSMVLVIQMFMLLTGALIIIL TKTNPASISKNEVFRSGMIAIVA VYGIWMAETMFAPACYGYI LPTYPSDLAAIQFDRSGTTHIGR FVINHSFILPGLIGVSVCVFGWI FAAIKRDAAAGRAKENVIFHHF PFQSVKADIATNPFKRPGGAFIR ITQFRTVQTFRLSAYRLDFAG DRLRISTPRAKMRTAFKKDHLR QRRRCIRQAPPARHNLVGAV ALPATVAGVNFTFSNPLDSSV LSLLTDFSTAVGSIVMLAVIM GLMLAFDMGGPVNKVAYAFM LICVAQGVYTVVAIAAVGICIPP LGMGLATLIGRKNFSAEERETG
13717	44085	A	13797	3	2185	
13718	44086	A	13798	1	920	

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13719	44087	A	13799	251	479	TQRVDWRSRSSISPGDGLHAFP AFGKEGGKMLDRLRERRDVKT LQSGSAAAGAEFALAGAHPT GTTA*IQAINV
13720	44088	A	13800	1	939	
13721	44089	A	13801	1	386	
13722	44090	A	13802	3	524	
13723	44091	A	13803	1	548	
13724	44092	B	13804	67	1144	
13725	44093	A	13805	811	974	VSRRIKLDVTEEFARAGDNKRC ICQ*RHGLAERDIARLLVEIVVI WCDIGVIAQ
13726	44094	A	13806	1164	1262	
13727	44095	A	13807	2	894	
13728	44096	A	13808	1	1587	MVKEGTFREDLFYRLNVIHLIL PPLRRDRREDISLLANHFLQKFSS ENQRDIIDIPMAMSLTAAWSW PGNIRELSNVIERAVVMNSGPII FSEDLPPQIRQPVCNAGEVKTA PVGERNLKEEIKRVEKRIIMEVL EQQEGNRTRTALMLGISRRAL MYKLQEYDATGFFRDMGTIMV GGFMGIGTPSRLVEALLESQVR DLTLIANDTAFVDTGIGPLIVNG RVRKVIASHIGTNPETGRMRMSG EMDVVLVPQGTLEIQRGCGAG LGGFLNPTGVGTVVEERQTSID TSTRKRPFELGRPSRNNDKGIRP VDQALDRKNIRE/ALHDSLKRLQ TDYLDLYQVHWPLRPFYCFGK LGYSWTDSPAVSQDLTDLAL AEYQRAGKIRYIGVSNETAFGV MRYLHLADKHDLPRIVTIQNPY SLLNRSFEVGLAEVSQYEGVEL LAYSCLGFGTLTGKYLNGAKP AGARNTLFSRFTRYSGEQTKQA VAAYVDIARRHGLDPAQMALA FVRRQPFVASTLLGATTMDQL
13729	44097	A	13809	1	618	

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13730	44098	A	13810	80	952	RPGIVALNAILPLSRTRQSKPTR LKKRAIANCAPTWKKRFVALV YRTA*RFPSITLSVAVT*PASAK NKAIKMTQKIEQSQRQERVAA WNNRAECDLAAFQNSPKQTYQ AEKARDRKLKANLEAIRRSG LQDGMTVSFHHAFRGDLTVN MVMDVIAKMGFKNLTLASSSL SDCHAPLVEHIRQGVVTRIYTS GLRGPLAEISRAYCADSHHGP FAMVNNMTDLTAQEPAWQTR DHLDDPVIGELRNRFQPDFTV QATRTGVPVVKREQLLEV GDFLKKLPKPYVMLFDLHGMDE RLRTHREGLPAADFSVFYHLISI DRNRDIMLKVLAENDLHVPT FTKLFPNANWYERETWDLFGIT FDGHPNLRWIP
13731	44099	A	13811	92	735	RLRLPLQPRESSVLPGLTTFHAS STSETRQSKPTRLKKRAIANCA PTWKKRFVALVYRTA*RFPSIT LSVAVT*PCVNIITIGQVKT VTIATAQIQRTFRNFHSRFQYFR NSPKQTYQAEKARDRKLKANL EEAIRRSGLDQGMTVSFHHAFR GGDLTVNMVMDVIAKMGFKN LTLASSSLSDCHAPLVEHIRQ GVVTRIYTSGLRGPLAEISRGLL AEPVQIHSHGGRVHLVQNGEL NIDVAFGLVPSCDFEANGY TGKACCGSLGYAIVDADNAKQV VMLTELLPYTDNPEA
13732	44100	A	13812	1	1113	
13733	44101	A	13813	5121	6228	LRRDSGRLRSCWHPRSPSTMG SLGQREDLQEDRNSGADPGQR GRCSIHLEGGPGQPCQLQRAVQ GEGDPVLAKEEIQDQCHPHGQV QLLLVPAEPPVRAVPPRVQPV LPHHHHPAELSGIREE*GNQND AEN*TISTRTGTSGLESSR*M/SILP LSRTRQSKPTRLKKRAIANCAP TWKKRFVALVYRTA*RFPSITL SVAVT*PYWSGAPGPGCRPPYC HFRHRGARGSGAPGDGGEAPP AAAFGGDVGFGL
13734	44102	A	13814	56	196	CRGDGGLIHCQRRMG*PCG* LRQRKAELFQHLPLC*FWRPEI GTVCSGSIDNGSDRLRR
13735	44103	B	13815	64	2373	
13736	44104	A	13816	3	403	
13737	44105	B	13817	55	1040	

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13738	44106	A	13818	587	1533	VLLTAKFFPSMYSPIKTAGGPA ST*VL*MIISIDAEKAFDKIHQPF MLKALNKSENKIPRNPITYNGCE GPLQGELQTTAQGNKRGYKQT QQHDMHMTKNQYHENGHTA QGMKGITQPSAFIPTAESNSFQP QVKTLPSPIDAKQQLQRKIQKK QQEQKLQSPLPGESAAKKSESA TSNGVTNLPNGNPSILSPQIGIV VAAVPSPIPVQTRQLVLTSPSP MSSSDGKVLPLNVQSHQNCW WTRFNMSLNVVKMTTISLTPS NSNTPLKHSASFISATGTTEESR SVPQIKNGSVVLSQSPGRSSSA GGTSAVEVKVEPETSSDEHPVQ CQENSDEAKAPOTPSALLGQKS NTDGAQKPSNEGVEIKATKE RRSSPATEQSWMENVFEEQREE GFRRSNHSQIREDSQTGKKEEK RLKELMELKTKVRELREECRL RSRCDQLEERVSAAMDDEMNE KREGNFREKRIKRNEQSLQEIW DYVKRPNLRLGVPESDGNGT KLENTLQDIIQENFPNLRQANI QIQEIQRTP
13739	44107	A	13819	590	817	
13740	44108	A	13820	107	410	KGRNIQNGPSSRVSLWRSLYF LNLNTGLPC*IGEVLLDNILQSV FQLGSILPITFRYTNQT*1WSFHI VPYFLEALLISFYFFSKLPFSLH FIHFIHFR
13741	44109	B	13821	1	3735	
13742	44110	A	13822	922	1137	HFFLHFNFGESDNYVSWSFSSR GVSLWRSLYFLNLNVGLPC*IG EVLLDNILQSVFQLGSILHITFR YTNQT
13743	44111	B	13823	1	954	
13744	44112	A	13824	3	156	
13745	44113	A	13825	683	972	SHRLLRLHSSRSSPGLVSSSISS FKHFSVLVILFTLMIVSFAVQKL FSLIRSHLSILALVIAFGLVLM KSLPTPMSSMVLRS/SSF*GFYG FRSYI
13746	44114	C	13826	1	895	
13747	44115	C	13827	372	1727	
13748	44116	A	13828	705	1072	LALLVELIPLPLCNGLLCLF*SL LV*SLFYQRLGLQPLPFFVFHLL GRSSSILLF*AYV*LFWHDFAA AGTGCSFPCLALPSGALVGQA WW*QKSLICLSVKDFISPSLM KLSLAGYEILG

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13749	44117	A	13829	1	1136	
13750	44118	A	13830	547	675	
13751	44119	B	13831	144	1877	
13752	44120	A	13832	1	441	
13753	44121	A	13833	27	344	
13754	44122	A	13834	287	600	GPGLQSSPLLSPWPWRASSPLL LRPSVRGWHLGEP*NCFPSPLA AS/EQAPKRSS*PQCNHR*RETA ARGLAYPPDRPLPSMLSCESPE TPAKAGPGRERGCEKC
13755	44123	A	13835	2	226	
13756	44124	A	13836	2	226	
13757	44125	B	13837	45	518	
13758	44126	B	13838	1	699	
13759	44127	A	13839	3	362	
13760	44128	A	13840	2	130	
13761	44129	A	13841	3	96	
13762	44130	A	13842	1	545	
13763	44131	A	13843	2	144	
13764	44132	A	13844	2	91	
13765	44133	A	13845	1	370	
13766	44134	C	13846	1	214	
13767	44135	A	13847	215	310	
13768	44136	A	13848	2	91	
13769	44137	A	13849	1	289	
13770	44138	A	13850	1	997	
13771	44139	A	13851	1	192	
13772	44140	A	13852	2	267	
13773	44141	A	13853	2	181	
13774	44142	A	13854	1	171	MESYAAIKNDEFMSFVGTWMK LETILSKLSQGGQKTKHCMFSL TDVIARRRSWTSI
13775	44143	A	13855	92	244	KRRRRRGQIRKMKEEENRRT WMKLETILSKL*QRQKTKHRM FLLIGGN
13776	44144	A	13856	146	382	
13777	44145	B	13857	124	1215	
13778	44146	B	13858	1	628	
13779	44147	A	13859	377	484	
13780	44148	A	13860	2	220	WARTSCLKHQKQWQKPKLA NGI*LN*ASAQQKLPSEWTG TWMKLETILSKLLQGGQKTKHR MFLIGGN
13781	44149	A	13861	965	1150	GVDQRAVCSSRIW*SHLFLFHS VVVHLPWAGTWMKLETILSK LSQGGQKTRHRMFLIGGN
13782	44150	A	13862	254	571	YSYKLEIIIGKQPEIYRDCYRP AV*SQTAVLASEAPWA*DLPS QVSDTISWWTVC*AHWKSAVL GWE*PGFPGTWMKLETIVLSLK LSQGGQKTKHHMFLIGGN

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13783	44151	A	13863	62	214	
13784	44152	A	13864	274	435	
13785	44153	A	13865	1	294	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSLVYIFFLDEFM YFAGTWMKLETHLSKLSQGOQK TKHRMFSLVGGN
13786	44154	A	13866	663	1266	PPLTCQCSHLCLVTLVGH/WIKLE THLSKLSQGOQKTKHRVFSLIGG AGALAKECMSLYPGCKITVFDI PEVVTWAKQHFSFQEEEQIDFQ EGDFFKDLPEADLYILARVLH DWADGKCSHLLERIYHTCKPG GGILVIESLLDEDRGPLLTQLY SLNMLVQTEGQERTPTHYHML LSSAGFRDFQFKKTGAIDAIL
13787	44155	A	13867	1	681	
13788	44156	A	13868	1	247	
13789	44157	A	13869	2	178	
13790	44158	B	13870	1	2042	
13791	44159	A	13871	1	378	
13792	44160	A	13872	1	683	
13793	44161	A	13873	1	972	
13794	44162	A	13874	308	406	
13795	44163	C	13875	177	653	
13796	44164	A	13876	1	465	
13797	44165	A	13877	3	1175	FFSQAAALLVVLGSSHTLQRA RKHSAPGLPDTCALLQPPAASA AAAPSMSPDVPETPSAIQICRIM RPDDANVAGNVHGGTILKMIE EAGAIISTRHCNSQNGERCVA LARVERTDFLSPMCIGEVAVHS AEITYTSKHSVEVQVNVMS ENI LTGAKKLTNKATLWYVPLSLK NVDKVLEVPVPPVYSRQEQEEE GRKRYEAQKLERMETKWRNG DIVQPVLNPEPNTVSYSQSSLIH LVGPSDCTLHGFVHGGVTMML MDEVAGIVAARHCKTNIVTAS VDAINFHDKIRKGCVTISGRMT FTSNNSMRFKVLLDPAPVVD S FQKRYRGRQCLSS*VSLSQER QV/PLPVPQLVP/ETEDKKRFE EGKGRLYQMKAKR/QGHAEPQ
13798	44166	A	13878	121	361	SLFELENRSKFSVATAGLVPSR RLSINCIRRAFITSSNGFPLWFCL HQKGPVDCCVAVY*CGTEDGS WAPTHPGVGPSLP
13799	44167	A	13879	1	462	

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13800	44168	A	13880	3	287	PCSLSSDCCASNQRDSVIGIPSE PRVGYNILVIRFLSPSEKRSR\IV GVTRFSSAWEPSQLAGILPISEP PSNRIFACWGKPAWTACCNLSLR ARR
13801	44169	A	13881	1	1332	
13802	44170	A	13882	1	753	
13803	44171	A	13883	1	516	
13804	44172	A	13884	71	277	IYFNTQESFCPPRPLK/LCDGRG CHKGL*NAFKAFSPFSWPLALG SFLLMQISAACLNSFPENGLFFS TT
13805	44173	B	13885	1	1095	
13806	44174	A	13886	1	741	
13807	44175	A	13887	264	2880	WLLQKHKLHVSRLGLPDTSW ILPSRPDAGGRFPRTPPCVL VV HKPSRHCREWTA NTVPK GAL AKWLLEPKADLQGWHL PADG QYTKPSISYNIKLYINCYNRTVT TAAQHQQVQRKHGASIFLAEN VAVREKDKEEKVTRAPTEQA WTAGSWIETAYREIKGVGQES VCITVMHLEELVYELAWIUMSA VVEAFDPVAPSSKRLNPD PDP YCCTPYTLHTSPPPSPCTPYT LHTGPPPTPFCTPYTLDTSPS PQTHSCCTPYTLHTVPTFHLPA AHPHLLHTIPPQTQGGQFVSED EYLEISDIKRDQSGEYECALND VAAPDVRRKVKITVNYPPYISKA KNTGVSVGQKGLSCEASAVP MAEFQWFKETRLATGLDGM R IENKGRMSLTFFNVSEKDYGN YTCVATNKLGN TNASITLYVD HIVGSKALLSKCKRTEIITNYLS DHS AIKLELRINKLTQNHSTTW KLNNPLLNDYVWHNEMKAEIK MFFETNKNKDDTTYQNLWDAFK AVCRGKFIALNAHKKRQERSKI DTLTSQLKELEKQE QTHSKANR RQEITKIRAELEIETQKTLQKI NESRSWFFERINKIDRLRLRIK KKREKNQIDAIKNDKGDITTYT TEIQTITREYKYKHL YANKLENL EEMDKFLDTYTLPRLNQEEVES QNRPTTGSEIVAINSLPTKKSPG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13808	44176	A	13888	1	629	AMAGSPPASLLPCTLISDCCAS NQRDSEVGVGPSEPGVGYSLVV RRFLSPSEKRSIRVGVTFRSRR PSPLSLTQKGNSLTWSAQVLT PAPEKQPDNKLPLPRGSRDPT EYFHGQEVDRKSDHEVHDHVSQ IHSFRDEVKRLGAEDSSNAETP TELHEFNTGGVYRPPNSTSVIQP LDQGVIRTFKPCYTKYSLEKIVS AVEENPDRT
13809	44177	A	13889	1	1452	
13810	44178	A	13890	167	309	
13811	44179	A	13891	3	386	SVGALQKQGGWHQRRCSLHF PSFLCVFSLAKSRRADHNQDPR ASRMASFSLTSSPLARSAASAVA AFGGCTSGNGRFSSVP*AYRQV FQRIAIAYVGPLMRDR*AHPVK TPDAIDCRIRQPAIPRLQ
13812	44180	B	13892	121	298	
13813	44181	A	13893	473	1826	
13814	44182	A	13894	1	270	
13815	44183	A	13895	3	3706	
13816	44184	A	13896	1	1464	
13817	44185	B	13897	591	729	
13818	44186	A	13898	1	1326	
13819	44187	A	13899	1	1152	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13820	44188	A	13900	1	2524	MREEFAHRWLRAGEKTPFDA LEKLTDPMLFAAAMVSAGKAD VCIAGNLSSTANVLRAGLRIGL QPGCKTSSIFLMLPQYSGPAL GFADCSVVPQPTAAQLADIALA SAETWRAITGEEPRVAMLSFSS NGSARHPCVANVQQATEIVRE RAPKLVDGELQFDAAFVPEV AAQKAPASPLQGKANVMVFPS LEAGNIGYKIAQRLGGYRAVGP LIQGLAAPMHDLSPIAATDAG SAAQIRIGDLVSVHVIRPHVD LEQVFPGLKAYTATCNHPVSL RFTIKSSDRIKLSNQTLSKSNL FIMRFYCFSLCLSLSAFYHCRGV IVNIQAVFWLQKGTEAADILTT CAQLWIMMYALLSVFSLDVL NLAQKFPAASQLPLKGIFQGIKL IGAILVGILMISLLIGQSPAILISG LGAMAAVLMVFKDPILGLVA VRNWDNTITTTPTWSLVSDSFK NWSGMSASGGRRIKRSISIDVTS IRFLDEDEMQRNLKAHLKPYL TSRHQEIENWNRQQGSTESVLN LRRMTNIGTFRAYLNEYLRNHP RIRKDMTLMVRQLAPGDNGLP LEIYAFTNTVVWLEYESIQADIF DHIFAIVEEFGRLRHQSPGTGNDI RSLAGVTINKAPGDDEILKNTV DFVSFSYYASRCASAEMNANN SSAANVVKSLRNPLYQVSDWG WGIDPLGLRITMNMMDRYQK
13821	44189	A	13901	1	2370	
13822	44190	A	13902	1	282	
13823	44191	A	13903	1	714	
13824	44192	A	13904	3	506	
13825	44193	A	13905	459	551	
13826	44194	A	13906	401	492	
13827	44195	B	13907	479	702	
13828	44196	A	13908	120	256	

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13829	44197	A	13909	16	1249	SKSGAIEIARLAGRVHGVVVQI TSEIGPLTLLTANFAFSAS*STA WKATSMDEGVLS*YSTASAS AERQSTHQ*TGFAPLCR*PLPMI /VAQRADDVGFSEVHGQVRV RPVAQHAQTDKVFALTYNLGR RVFAALGAELGGARSAVRPVP ECYAVRETLALLQKIFPIRQCEN SVYRNRSRFLQYQIGRCLGPC VEGLVSEEEYAQQVEYVRLFLS GKDDQVLTQLISRMETASQNLE FEEAARIRDQIAVRRVTEKQF YSNTGDDLDVIGVAFDAGMAC VHVLFIHQGKVLGSRSYFPKVP GGTELSEVVETFGQFYLGQSQ MRTLPGEILLDFNLSDKTLAD SLSELAGRQINVQTKPRGDRAR YLKLARTYAATALTSNFRSIYR SPATDRACQRVETAGNER
13830	44198	A	13910	1	438	
13831	44199	A	13911	1	1200	
13832	44200	A	13912	1	300	
13833	44201	A	13913	1	431	
13834	44202	A	13914	2	1465	
13835	44203	A	13915	1	513	
13836	44204	A	13916	3	535	RDKILVFKDENFWMIRGYAVLP DYPKSIHTLGFPGRVKKIDAAV CDKTRTKTYFFVGIWCWRDFE MTQTM/EKGFPQVRVVKHFGPISI RVDAAFQYKGFFFFSRGSKQFE YDIKTKNITRIMRTNTWFQCKE PKNSSGFGFDINKEKAHSGGIKIL YHKSLSLFIFGIVHLLKNTSIYQ
13837	44205	A	13917	1	876	
13838	44206	A	13918	23	414	
13839	44207	A	13919	2	425	QERGPHQVIQRKECLREYSPVV S*AKGTGVAVGQKGTQLQCEAS AVSSAEFWYKDDKRLIEGNK GVKVENRPFLSKLIFFNVSEHD YGNYSVCVASNKLGHNTASIML FGPGA VSEVSNGTSSRAGCVW LLPLLVLRLLLKF
13840	44208	A	13920	1025	1270	
13841	44209	A	13921	370	701	
13842	44210	B	13922	1	660	

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13843	44211	A	13923	1	432	RFSRVDDFVLTMDDGPPRRAR GDLTHSGLWRVCCIEGIYKGHC FRINHFPEDNDYDHSSEYLLRI VRASSVFPILSTILLGLLCIGA GRIYSRKNIVLSAGILFVAAGL SNIVGIIVYISSNTGDPDSKRDE DK*NHYN
13844	44212	A	13924	1	1093	
13845	44213	A	13925	1	1203	
13846	44214	A	13926	1	1353	
13847	44215	A	13927	2	445	
13848	44216	A	13928	1	227	
13849	44217	A	13929	1	840	
13850	44218	C	13930	120	356	
13851	44219	A	13931	40	342	
13852	44220	B	13932	403	473	
13853	44221	A	13933	70	2169	
13854	44222	A	13934	1428	1905	RCAATSGYGERVQRITV/PTHV W*ASLSQSSAHRVVAINSIANK RSSMPPKSWATVALTSTKLKCR FMAKVRNKSFSLVHNV*MTISI/ SPWVILSSGVDEKLPRAVRVA MTAGASGFLAGRAVWASVVG LPDNELMLRDVCAPKLQQLGDI VDEMMAKRR
13855	44223	A	13935	227	342	VHSWQRYSGR*RGY*PQNQSA TDQTRRWQSLKTAGAVA
13856	44224	A	13936	480	928	FFADLQQPVCADSYPLLVMQK LAPHKS*NAVWQRSATKSFSV L/AQGLNDHINMPWVILSSGVD EKLFPRAVRVAMTAGASGFLA GRAVWASVVGLPDNELMLRD VCAPKLQQLGDIVDEMMAKRR FIPLLRWVDLALTRWLITVSK
13857	44225	A	13937	564	1185	WLHASAALLRW*YQLPGQPHH RRCRSADGSHVPSLCAAVPDQR VPLITVRRIGMQAMTTSTTGDRQ RSWQIAMDGSQKLQRMMLDSV RWHLAHDSKFDLLALGVAGW MRYVGGVDEQGNPIESDPLL RMAANRFVHITQLPVIYRAFRN SFTQVARIQLCHKRFQQRHTSV REQIVTVLSGIRDNVHVFVQTL TGDGVGNQRLVQ
13858	44226	A	13938	228	424	HRFCPAARH/RSWSGLREMAVS ISMRRRIINSGRYCAICWYKRRS RCARNMLIFVARSTPIPGPS
13859	44227	B	13939	128	1670	
13860	44228	A	13940	2	2367	

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13861	44229	A	13941	1	921	ELPASPAPCARTPQPLGGRWEA ARRKERVLCDFVDGTLTPAR/ QGRITLKIGSSHRECHADTPAE CGVCSSVTEVRAKWSQTC*KP ECYASPLPP*KIDPEVA AFLQKL RSSYLPVGSQTWSHTLSSSCPLC DPEVIGRDTVPVSGSGSPGHAQ SPVFLGQTIQNLGPGGARFEF RA/CSGSLWLALPHH/RGT FIEF RNGNCVPSPQGLAHSRSELPSA PSPLQKEQAALLALASPPSRE* QSPPLPTGGMISFDFPEGWOK QVRSSQCGEGLHNLNIPPLPILCV QGGNDFEIFADPRTVGHS
13862	44230	A	13942	105	416	HSVLEVGPWVEVFGSWGQILH SLVSSHVRHWLLPSPSAMTES SLTFQKQPSRCQHHASCKAYHS HQLLLVPTAGRLEDRSHH*IPC KHSPAPAWSLAAPVGN
13863	44231	A	13943	191	573	SSSGGYQQLMRVIGTRDTAV NKASNVPSFGA*/IPSGRGQAK LIALTRALTLAKELHVNIAAC KYAFHILHQHDVIAERGFLTV QGSSSIINASLIKTLKATLLPKE AGVIHYKGHKASAPIA
13864	44232	A	13944	1	1065	
13865	44233	A	13945	321	537	
13866	44234	A	13946	346	1260	GGPARAEFSRHLGCKGHHPLPK DVASEVPAGSSTSVSLIRTNCG PGLGSWEPP*FFSENKRLSTLMS FTLRDSKMFSQSGFLGCSAG EHSALRDPTASGLPGTASGVRP GR/RQRVGS DIEASTQGESKPCI LSI*TL PNA*LKTKLTLPLEAAC TNPHFSITARIGPAHLAAPRPV TPAGRGRGARAPGR*CAAAARPPP ASQ*VSGSPAPGGGSPYAPAAAR TS*PSSLAPGAKRLRFSRVATFC CSFLAWSSSSNKAFC*EHMSL LSSWISQSLKVASCCPCEQFDS WKRENILLFS
13867	44235	B	13947	1	459	

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13868	44236	A	13948	63	1263	V E A A K K A H H A A C K E E K L A I S R E A N S K A D P S L R P Q A H T Y A L S P L F L T A M P S V * Q G E H V I Y T R V R H S D Q V S E S S G K L S L P L E P G I W A F E A A Q V P P R W D Q V R S L E P T T E W E A P G L K K R R V S Q G L N G N E P L S C A W I F L * T K E Y E K S L K E L D Q G T P Q Y M E N M E Q V F E Q C Q F E E K R L G W D K G * L A P A F * K S H V S L * F S Y K A I Y H D L E Q S I R A A D A V E / D R R G F R K * * T F G F S P S A P V A * E W S A D L N R T L S R R E K K K A T D C Q D P H G P L Q S W D P L K A L S L H S T L N V P S N P A Q S A Q S S S Y N P R G P H T L C R P V L R A L W P L S C S V S S Y E K T Q S Y P T D W S D D E S N N P F S S T D A N G D S N P F D D D A T S G T E V L C S P P S V S Y L S W R R L P L C L A G D E L T K M E D E D E Q G W C K
13869	44237	A	13949	2	485	A A A F G T R L S R R G R G C G V T G S G G G R R R V P A P R R P S P L Q P P H Q / P P R R P S R R T P G C G S R G A / P S R G R R L V P P P P E P P R A A Q Q R A R H V R T S / R P A A R Q P P R R P P A Q P R S C P R R V R P T P A W S P P G R R G P R R S R R R R R R G G R A R A R R P R R R G Q V P R P Q S A T G A G H A R
13870	44238	A	13950	1	207	
13871	44239	B	13951	1	5297	
13872	44240	B	13952	1206	1360	
13873	44241	A	13953	46	369	N E G K N A K G S Q R E R S G Y P Q R E A H Q T N S G S L G R N P T S Q K R V G A N I Q H S * R K E F S T Q H F I S S Q T K L H K * R R N K I L Y R Q A N A E R F C H H Q E G S T K H G K E Q P V P A A A K S C Q N V K
13874	44242	A	13954	476	868	K Y D C C I S S T F C R A L V H F S R T T F Q V N S P L S P N I S A F G Y M P L K Y S I Y F L H H L R P N I L * A A S Y F L K Y K G T L K L P A L R G C L S * S T R C W C K I H I C I * N D / E C L Q F L G P W F E N E F C F L P S T S Q F V E F V L D I L V L Q N E P

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13875	44243	A	13955	1770	3003	PANIIMTGSINSHITILTLNVNGV LNAPI*RHRPAIA/S/WLSQDPS VVVICIETHLTCDRDLTHRLIKG WRNIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMAK GSIQEEELTILNIYAPNTGAPRFI KQVLSDLQDRDLDAHTIIMGDFN TPLSTLDRSTRQKVNKDIQELD SALHQADLIDYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALL SKCKRTEITITNCLSDHSAIKLEL RIKKLTQNHSA TWKLNLSLLND YVWHNMKMAEIKMFFETNENK DTAYQNLWDTFKAVCRGKFIA LNAHKRKQERSKIDILTSQKE LKKQEQTNSKATRRQEITKIRA ELKEIETQKTLQKKQPNKDPAM EKNKNTDRVLARLIKKKREKN EFSAHILYKFSKQNGS
13876	44244	A	13956	105	392	RSRKPRGNPKSHPEDTDPTKAP RKQRQISSRGHRSR*EPGPQSA PGFREQRRRGQMG*IWYLTPT PGGQRPSSAASPRGFPTNNSR LPAAEPE
13877	44245	A	13957	55	403	SEGMSGKASEKQEAFCPRHLT RAVDGPS*SGLLGSRLPPSCSPG KEAPGGSELYLCLMRGLQTL*A RSGTGLR/PNPAEIR*EPGPQSA APGFREQRRRGQMG*IWYLTPT PPGGQ
13878	44246	A	13958	217	444	RSRKPRGNPKSHPEDTDPTKAP RKQRQISSRGHRSR*EPGPQSA APGFREQRRRGQMG*ITPCRP ALPKSKPRPL
13879	44247	A	13959	309	670	PCPRASSQGLKATHGQR*SSEP PGASFGLQDGGRRPRRPD*D GPSTGLVRCLGHANVGDPLK VFVFFKNLSPTYLRASAEQTLPL LLPLHLGLCLHQLHLGFTAA WAQLTFWEASQ
13880	44248	C	13960	392	760	

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13881	44249	A	13961	24	915	HAGRHRGSLFPGARPSETRAH CVRTARPNCKEEDTPMVRGKN SGGEHCTWGPSLAAGG*GIGDP GGLPGTTPHPLQLLLHGFAGP HMASLCCGVSSPAGVQRWPA* GSGNHQVKS WLGLPKNV S*AP SML*NPQMQLMKAQPHGRCE VRRGRVCSALGP/IGMSGKASE KQEA*DEGHPHLHAPGT*QDQ VDGPS*SLIGSRLPPSCSPGKE APGGS ELYLCLMRGLQTL*ARS GTGLRANPAEIR*EPGPQSAAP GFREQRRRGQMGIWYLTPTTP GGQRPSSAASPRGFPLV
13882	44250	A	13962	397	612	RPQHHTFCCDGRVMMARQKGI FYLTFLILGTCTLFFAFE/CSFG *VELPDYGYFGSRGRTCFGLSL GLVLG
13883	44251	A	13963	125	1298	FQSWAQPLFLLSCNRKTHFGTR IPIMSVMVVRKKVTRKWEKLP GRNTFCDDGRGMMARQKGI/ YLTFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSMAT L/LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGRPPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHC PW VGCNVCGRNRYRYFILSLSL LTIYVFAFNIVYVAIKSLKIGFL ETLKETPGTLEVLICFFTLWSV VLTGFHTFLVALNQTTNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVL CGPLPPSVLDRRGILPLE ESGSRPPSTQETSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPPEP PEPPQEA AEAK
13884	44252	A	13964	44	647	DYSAQHGKASQKHVARLISSGT FQGATVSRPFQLSTSSSFCSSSS SLSSSSSLSSLLSCSSSVFLS LSFFFCSEASFLPFC SRLYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFFIAKLLAQDVAYSTKT LAAREIGAPGLLDVDVTRELR GDRG*AKLPFQHLPSPCPFVRPP RAAHRLLDDPGDHGIGQV
13885	44253	B	13965	158	1075	

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13886	44254	A	13966	125	1297	FQSWAQLFLLSCNRKTHFGTR IPIMSVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKGI YLTFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSMAT L/LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGORPPRIK NFQINNQIVKLKYWYTKIFRA SRASHCSICDNCVERFDHPCW VGNCVGRNRYFYFLFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTVLEVLCFFTLWSV VGLTGFHTFLVALNQTTNEDIK GSWTGKNRNVQNPYSHGNIVKN CCEVLGCP.PPSVL.DRRGILPLE ESGSRPPSTQETSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPPEP PEPPQEAEEAEK
13887	44255	A	13967	247	850	DYSAQHKGKASQKHVARLISSGT FQGATVSRPFQLSTSSSFCSSSS SLSSSSSLSSLLSCSSSESVFLS LSFFFCSEASFLPFCRLYASRA SFNGVTNRVNSISSMAESTSLA FSVFRFPFIKLLAQDVAYSTKT LAAREIGAPGLLDVDTVRELR GDRG*AKLPFQHLLPSCPFVRFP RAAHRLLDDPGDHGIGQV
13888	44256	B	13968	298	380	
13889	44257	A	13969	48	252	QRAGSPHSPRSLAPLPPLPLW RHLRSPSAHRCTVGAFWDGQ G/LEPAPSAALAAFPISRARDLQ LA
13890	44258	B	13970	1	447	
13891	44259	A	13971	236	559	MWLEPMQMGLHMMMEKMAA RTSAILD*GTLK*FHFTLTSLK ALSSHTPIFPGTGELQLPVSPV CLDQGMQLKPSTSSHLLKTVKP RMKRQSLHMKQSFEPKIYL
13892	44260	A	13972	1	645	MKPQTLTVSVTAFKVAHLEFVP SDVQMCSEFLPSGGFVVSLSAG VKLQTFVAVSFTAHKSSVDPKNS EAQLASPSGFCTRAADGAACQS LPCTCTPQPLGGRWDWALWS RGW/LLVEEA WAAQEPTEELRE RALALASPERGSHSAVVGQAP QVPPKWEPRQRRRRERARAVR TASTLSPLNPPSKQDITLTVGN LADHSSYFLLDRGEGEALQL
13893	44261	A	13973	28	322	
13894	44262	A	13974	1760	4426	
13895	44263	B	13975	942	3414	

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13896	44264	A	13976	1	274	
13897	44265	A	13977	545	1150	RISGPGAVLLPVPMPALWRLRHR MFSLTKK*HLPAPHRSLAEGYLL YQPQLDTLKARLTQKYQELQV LFEAYQIKKTKLDRQSSASLET LLALLQAEGAKIEEDTENMAEK FLDGLPLDSFIDVYQSKRKL HMRRVKIEKLQEMVLKGQRL/S TRPWPRCPGCPNWHLPFPPT LPQSQWASCRCTSAHPPTTPG AAGRL
13898	44266	B	13978	213	611	
13899	44267	A	13979	1	639	MEAVTVVPVGTTEEGMGEEQD SGTTTGCGLPSVEKMLATNPGK TPISLLQKYGTTRIGK\TPVYLL KAEG\HQPNTFWV\VGNTSCT AQGPCKKVVVKHAAEVALRHL KVESMLEPAPEDSSFSPLDSSL PEDFPVFTAAAAATPVSSVFLT RSTPMEKQPPLL\QQSECIPVG ALQKLVVQKGWWLPEHTVT*E SRPDQHEELT*RVERFT
13900	44268	A	13980	361	894	AFFPMSTAGVCGNVEGEPETP WSLPLSQVPFSPNA/CPQGTGLGR S*AGVAGAPGPGVPGRSPAA/GI PEPAARPGRPALSRPLGLGGAG ARSGAA*G*GSRPGG/PLPADP VQSWG*EAPSH*PGTSADSP PSGVSGATGDCLWGSRAELF GFATTSSAAPFGLPTFFFPVSP
13901	44269	B	13981	1	3842	
13902	44270	A	13982	3	407	DAWAAARPGRSCALPPPAGA/PE EPGHVPGAAG*G*GSRPGGRFQL PDPVQSWG*EAPSH*PRNFQ TRRHLGVKQHGCSQSPHGSRA SQAHPGISGLF/GPHHPGPPLFIH GPRCCCAQATASNHLFACGTSS DP
13903	44271	C	13983	127	297	
13904	44272	A	13984	3	1920	

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13905	44273	A	13985	3	2271	GQGRRTAGGGGGGAGVGAG AGAMEAERGPERRPAERSSPGQ TPEEGAQALAEFAALHWVSGE GIGVGSPAHTPADGNSGPQVFD AGEVFGIMQVEVEEEDEAAR EVRKQQPNPLAPPTSLCPMPTR QPHIVACARSIFLDHAWTCRV EHARQQLQQVPGLLHRMANL MGIEFHGELPIWVPEGSSGGW MGEREVPYVLCQTAEEKMPV WYIMDEFSGRIQHADVPSFATA VPLEEGPQSPVSPPLMGTH/DL GTEEVTRDFAYGETDPLIRKCM LPLSSSHRGMETPCVHTSRASL PLQACELPSWSLLINEPPRPAF PSLP*PHLYFRVCVSF*AIPGLVLE SRLDTWEPGSPSSGSPHRVYTD VQQVASSLTHPALPVRASRHC PPLELAHLPPPCRKLSSQERPGVL LNQFPCENLLTVKDCIASIARR AGGPEGPPWVVLGWHLGTQ APGAPQTALLPRGEDNHWICK PWNGLGCLVSGPRGLCPGHQR ACTCVLQVVSKEYIESPVFLRE DVGKVKFDIRYIVGGTSLAGTR PLKNPYVSAHLSSRAFAQGRRG RGGPTWSGWLLARDPARV*DL LSSLVHVSVERCPMQWALSEWQ LHHLSTWSSGLCGLAG**VFQM HRTPTP**QAACSRPSGGLYR A*WALCLLPGAADPLLRCGSEQ AS*LRLPGPQAEIFRAFTELFQV
13906	44274	A	13986	1	600	MEEQRVQFTLWLHFSPHGICQF ESGRQEAKKLKGSGQPLKTGEI KTGIQKYRREALQHYLGPSAL AGRSKALTGTAERSCSSGSDSI FTLCVNYNDSRAIMKTLAIGT GFDCAKAEIQLVQILGMPPER FMYANSCKQMSQIKYTANNGV QMMIFGNEVKLMSVARTHSKQ P/CHISVKS GAMLKASRLLE*A KEL
13907	44275	B	13987	1	2040	
13908	44276	A	13988	205	438	LYFLETGVFCVQVPAQQC*CSV PGSCRRPLEEAGWRGLGSGRL AGTGLPSGSRGNRTREGERGKL VRGRRGVTRWLS

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13909	44277	A	13989	284	632	KTGVFCVPGPRPTVLM*CSFVG GKKNQYCLTGDAGCLQEKHSL GPAGV/HLEEAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSFPFEP
13910	44278	A	13990	594	1003	VRKGHHAVRGLCGRAQFRCIS GDPGKRPLG/LPGGNAPKSGSL ARRPQPVRIQSRPQ/RGSVSHL GPAGVH*/RAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSFPFEP
13911	44279	A	13991	1	1500	VRVAHIPIAAEIAAIPDRGGHL SVGKRRLTFWFFYGVLPPFRDV AIEFSPEEWELDSAQQHLHRD AMLENYGNLVSLAAGDQSLPG DAAASAVCRQLSPSACGAILGL PPVNGVAPVLRGEIVTYTWSQ LTGLALALSKDGADGLRRLTRP TRRAPPALLAPQTAAERWRG KCDPRHGGGICALALQGWTLYP RESPSRESKELGGLWSFRADLD SRRQGFEEQWYPRPLRELGRG GRRPEARRWEGSGPGCRLLPL SAPELAPYRKLVNGLRGAGL GDGETGGTGEGRGRRRKRCC RTLSRDEGFNDICQDWLWRQF VGWVLYEQEVTLPQWQTQHLR TRVVLRASAHSYATVVSAAARS RQGRIGGLIYTLGMPFFLSGW QVPEPHAAGYVRECLIAGPLLM P/TTCCPLLISPVSAVGEWRGHA RA*GADSSSLVQNTDFDFNYA GLQRSVLLYTTLTYYIDITITT GVEHDSAEIPFPEYLRVNTGN
13912	44280	A	13992	2	307	
13913	44281	A	13993	220	427	MSTLPFSLQMFRRPPYGSPTC RSQDNRSYSRVTEELQERRRW NSGDAN*DQSPERRQRPHIE EAA

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13914	44282	A	13994	1	2832	MGKYYTQGDKVLMLAIQVH HACDGFHVGRMLNELQQYC DEWQGGAYPKGYFVQNTDFDF FNYAGLQRSVLLYTPTTYDDI TITTGVEHDSAAAPMVDSLAR VGVMARGNAITLPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLPSFLLTGQ QTPAFGRRVSGVIEADGSRRR KAAALTESDYRVLVGELDDDEQ MAALSRLGNDYRPTSA YERGQ RYASRLQNEFAGNISALADA
13915	44283	A	13995	1	2934	MITFDFMSHIQVTLMQEVSFHG LGQLRPGCFAGYSPPPGCFHRL ASSVCSFSRCTVQAAVDLPFWG LEGTSPLLAASLGSAPVGTLCG GSDPTFPSWTALADVLHEEGHT PASNFCLRNLAGESQSWRKE GLGTPRPTASSTEELQTLNEDSR LMTSPHINLETRDCDTELPKKS LGWKEIRVYGQNKTLGFWLQA QLLICDGGNLRMFRLPYGSPS TCRSQDNRGYGGVTEELMERK RWNSTDGFIHQGVLE
13916	44284	A	13996	68	425	SHILPGAPGAPAWWTRWPSTLP EPFPRGRGSPAGTSPISRPGLVQ SS*ASRGSDSRLPV/GPASCQAS GPGPDSRRPPCTPA/GPHHGSL PSAGRVGASAAAAGPPSPAVPL PPAERPAP
13917	44285	A	13997	324	723	TAFSLNFQGGVEGEVWAGTRA ARGACAGERGLGGSRTSGW/P GTAGPGQAGHGTCSLPCPSLPP AMGSCVSEPPRQAPPAPWRLV PSTAQGLRSVGTQCGTGGSSAC GPC/GDPGF*THQSAPCQNGPIS SL
13918	44286	A	14000	39	383	

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13919	44287	A	14001	181	1446	EDLLQEAAQLAEVTAQGKGLG QVRSLLDLSLEACAGSPPLQVLD LQDREPRSLTSLPSSAANRGLK EKAQSNPCGHRRHQAAGLKL LFSAQAPQGQPTAPRFRAATR KPGTAQSHAPLWSPAMSFPEL YFNVDNGYLEGLVRGLK/ALGE LSQADYLNLVQCETLEDLKLHL QSTDYGNFLANEASPLTVSVID DRLKEKMWVEFRPHEGTMYP EPTSPSP*TSITLQFT*FDNVIL WLIHRARLHRSIAELVPQVAH PLGISFEQMEAVNIAQTPAELY NAILVDTPLAFAFFQDCISEQDLD EMNIEIHRNTLYKAYLESFYKFC TLGGTTADAMCPTLEFEA/NR RAFINTVFFGATKTPVKDRCP AFFPH/CGAGFFPEGPAAMGFG LNNLLTGAKKRGYPNFPEVQL AFLRGDG
13920	44288	A	14002	1	1182	
13921	44289	A	14003	26	342	ARFLAGP*LPSRRTGLRDLQPA MPEPPPTPWAPVRPEPPRRAAP PAPRRPVSTGKEQTQGLRSA GAGHRDWQAAPAAPVRDPLG EASWAPESGGDVESLYV
13922	44290	A	14004	66	463	
13923	44291	A	14005	3	1446	
13924	44292	A	14006	221	852	NSFLMVGFPPFSL/CAAFDTKT GLRVAVKKLSRPFRLPDGYYTE FNIYLLNFYILTSSAV*VVLSH SVVIECLLSIRHCSRYFRKSSD KNFLRGSRLLCNFSLISRYLVTH LMGADLNNIV*RYR*YK**FFK MNSPFLPLPVGGELIMHHKVD VCFVFFSLPVYSK*QFVCSSAL *ILDFGLARHTDDDEMTAKGQPE CFVRWACAS
13925	44293	A	14007	55	784	RHIQDPASQRLTNWNSPKSVLV IKMMDASLLQPFKELCTHLM ARGAGGGHDARSLLTAPVSRE PPCRRVGSAGGMSRLALCFQEN MIVYVEKKVLEDPAIASDESFG AVKKKCTCFREDYDDISNQDIF ICLGGDGTLLYASSLF/QGNAA VVLRSRLKVRVVKELRGKTA VHNLGEGKSQAAGLDMDVVG KQAMQYQVLNEVVIDRGPSY LSNVDDVYLDGHLITTVQGDGVI VSTPTG

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13926	44294	A	14008	155	1592	PESRHQCFSDRSANFLTMEMEQ EKMTMNKELSPDAAAYCCSAC HVGDETSYNNHPIRGAKRSRL SASPALGSTKEIRRTSLHGPCP VTTFGPKACVLQNPQTVIMHIQD PASQRLHVEQRPRTVLVIKKM RDASLLQPFKELCCTHMEENMI VYVEKKVLEDPAIASDEISFGA VKKKFCCTFREDYDDISNQIDFII CLGVDGTLLEYASSLFGQPSP VMAFHLGSLGLATPISFENFQS QVTQVIEGNASCCSGSRLKGQ GW*RLRGKKTAVHNGLGKEK G/SQACRPGTMDVGKA/QAMQ VPRS*NEVVIDRGPSYLSNVD VYLDGHLITTVQGDGKARSTV LGP*ASLGRE*RLRLSLSGVIVS TPTGSTAYAAAAGASMIHPNVP AIMITPISRSVLTAGGPHLSLL DPQIMLSPEARNAGGGPFWKP WLRLLLSRPSISITTSYCLPSIC VRDPVSDWFESLAQCLHWN
13927	44295	A	14009	327	466	
13928	44296	A	14010	2	196	
13929	44297	A	14011	923	1776	WRKCGCETAGSASATRAAATE KMEAPRNKMRDQENSAWRN AVPGP*E*RQPEEFPRITSILAEP TVLSRRKCRPSEKRGSAATEKFG ATSAVTENPPLGAAGERANKTL GAATVTPTLGPRPRMEKGGTR CPSTL*PSVQERQEPSPSGNHPE TQKIEFAGRRVTFQHRWATTLR TRISGTGASPRDRSAFFGFPWC G/AAQPSDEESTPATQEEAQAQ AGVAAAASSEEPGHCAPRPPHA PRSALEFEDWSREPERSDDGDL ECRRPATPWRPPGSAWRLPCA A
13930	44298	A	14012	568	1223	SARGLLPGSGPLSHAGPQLQVE WFGCLPPDSTLELVVCGTVAI SRVRMSAVCVLRTWS/RNAG/Q L/CFTVFQPCSNVHVL/KGPNY VCFGGYPSFKYSHP/HNLFKTI NAVCGQLVQRFDPDTEEGIRK VTV/KCYVKEGDTV/SQFDNIGK VQSDKASVTIASPYDGV/RLK* HSLDDIAYVGKPLVNIEIEALK GTVNLFYQIDYCPFFVIGSQLK

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13931	44299	A	14013	5	296	LFSRVPSKGPPRYHHTSSRG*TR AD*LISS/IGNS*AHCIPSGLQGM LNLLPTPRAPVRPEPPRRAPPPA PRRPVPFDHPRACGTGRQLHLQ PRCGIH
13932	44300	A	14014	1	376	MQAVLLTVLQKHNQSVIYWY MKYIYYEGLVIMDDYDYVIMD YMTMETEKSHDLQAGGPGKPV VQFQFKPKILQASRGNGVKSWS KSKGLRTRCANVQGQENREGP AKHSPFLCLFVLFSSSTGRMIPN HTGDTSKVIAGTEERGVPKKVT LKFDACAIDRPWAHQLDCTY HFKGSNDEHDSRLHTNAG*L*L C/RLWIT*LWRLRNPMICRLEA QESQWYSFSSSPKSCKPVEAMA LSPGPSPKA*EPGVLMMSKGRKI GRAQLSIHLSSAFLFFSAPQOVE
13933	44301	A	14015	1638	2289	VEKKKKPMSAPALRLPLDTKLF TLVYVSETKKMAVRVLTQTVP WPRPVALLSKQLEDEVSKRWPP CPKSLVAIALLAQEADKLTLRQ NLNIKSPCAVVILINTKGHH*LM NARLARYQSLLEHPRITLGLSL QHNLNPATFLPVSESPVKHNCVE VLDSVYSYVGPNNRHDPLNISR LGAVTWMGSSFHQPLQSDTLK KTTSPGSSHTRKLGTGPRTAEA
13934	44302	A	14016	1	675	MAPPLRLPLARLRPPGMLLRALL L.L.L.L.SPLPLGLEIGELITPIGT SLPDLDPARRRWEIGIGRVGSE VADLCPGKEGGKVPEAEKEGV WCFSELSFVKEPQDVTVTRKDP VVLDCAQAGEVPIKVTWLKNG AKMSENKRIEVLNGLSLYISEV EGRRGESQDEGFYQCLAMNK/F *AILNQKAHLALSRIGST*RRRP DRP*EDEAFVMTTHCFQDLLTS
13935	44303	C	14017	18	329	
13936	44304	A	14018	391	895	WASSDTPTGFTQRWRPDWAGG GGGEERGDGTGVVWEGEKVY FRFRVTGGSSFPSPAVLVRAPN TGMPKLTYYQT*GPLGERGKEP VPPNPTLPQTFEGGLNASVVRK TEIPSPSPPPVCYLRAAERQ/PA GGSPQAKWRAASSPPPLPPVH LPPPPPPPPPPPPPP
13937	44305	B	14019	1	1110	

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13938	44306	A	14020	282	710	YPEPQGWVVAHTVQYPIHIQPL KPGPRGR*SIMDIQVPPKEGGV LILKNSSRLNNSWTQGCQISA FSPTSSLPGTPWSNVGPKIAP ITSFGE/PFIRVIWKQLPSWSIIQ V/SHKQ*QIHRVDIGWSPGQEC GPKGCFV
13939	44307	A	14021	1	1416	MIILDAEKAFDKIQQPFMLKTL SKLGTDTGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTQGGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSQY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQW/GKDSLFFHKWC WENWLAVCRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWLILKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHKMKCSSSLAIREMDIKTTMR YHLTPVRMAIKKSGNNRCWR GCGEIGTL
13940	44308	A	14022	1	3450	
13941	44309	B	14023	1	3171	

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13942	44310	A	14024	1	2433	MRTKTQHTRISGTHSKPVCRGK FIALNAHKRKQEKSIDTLTSQ LKELEKQEQTTHSKASRRQEITKI RAELKEIDTQKTLQKINESRSW FFERINKIDRPLARLIKKKREKN QTDTIKNCKGDITDPTEIQTTI REYYKHLYANKLENLEEMDKF LNTYTLPRLNQEEVESLNRPTG AEIVAISSLPTKESRTGWHRSR LPEVQGGTEKEGILPNSFYEASII LIPKPGRDATKKNFRPISLMNI DAKILNKILAKRIQQHIKKLIH DQVGFIQGMQGWFNIRKSINVI QHINRTKDKNHMISDAEAKAF DKIQQRFLKTLNKLGDGTYP KIIRAIYDKPTANIILNGQLEAF PLKTGTTRQGCPLSPLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL LSLFADDMIVYLENPIVSAQNLL KLISNFSKVSGYKINVQKSQAF LYTNNQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKDDTNKWKNI PCSWVG RINIVKMAILPKNWKKTTLLKFI WNQKRAHITKSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHTY NYLIFDKPEKNKQWKGDSLNF KWCWENWLAICRKLKLDPLT PYTKINSKWIDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLSFC
13943	44311	A	14025	1	1023	MGAIFYDKPTANILNGQLEAF PLKTGIQGCPLSLLFNIVLEV LARAIRQEKEIKVIQVGKEEVK LSLFADDMIVYLEDPIISAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNI PCSWVG RINIVKMAILP/KAICRKLKLDPL LTPYTKINSRWIDLNVRPKTIK TLEENLGNTIQDIGMDKDFTSK TPKAMATKAKIDKWDIIKLKSF CTAKETTIRVNRQPTEWEKIFAI YSSDKGLISRIYNELKQIYKKKS NNPIKKWAKDM/NRHFSEKEDIY AAKRHM
13944	44312	B	14026	1	2206	
13945	44313	A	14027	1	1689	

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13946	44314	A	14028	1	2523	MKQFLLYLDESNAIGKKFIHQDI DDTHVFVIAELVNVLQERCHTR LGYTEFLVAVRVTFGLCVAV TLHLKYQILIRGLLEMMFSFDA DILKQLPVTVPGLFPASLSPSSL LGNSPPSWLRHNSSEKVSVAVSS PSATKTLSTGIGKIDPGHKEMA EESSELLKNKMQAPPLSRCPESQ KCQHQRLRLHHWKPSVRHQVKR RSPAVLRSAMPADCPAVLEAT TATHPEKGTALSKHLPSDDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKQKQKGLDKKKKK GKLPKNYDPKLTDPDERWLP QECSEFYQGRKKGKKKDQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIPRH QRPAGAPATKKKQKQKKKKG GKGFVPLREITVVKVDTLVVFG ILEERLSVFHIIQYDTSYFPSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQQPFMLKTLNKFVGVDGY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNTV LEVLRARIRQEKEIKGIQLGKEE VKLSLFGAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTEQSIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL
13947	44315	A	14029	1	2868	
13948	44316	A	14030	1	3099	MGELITPLSTLDRSTRQKVNKD TQELNSALHQGLDIDYRTLHP KSTYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRINKLTQNRSTTWKLN LLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
13949	44317	A	14031	2	3419	

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13950	44318	A	14032	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFSSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRKIKNLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDDTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQKLEKQEQTHSKASRRQ EITKIRAEKKEITQKTQVKINES RSWFFERINKIDRLARLIKKKR EKNLIDAIAKNDKGDITDPTIEQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAEFYQRAIRQEKEIKGQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFFTELKKTTLNFIWNQK VRAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD
13951	44319	A	14033	845	1616	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWGRINIVKMAILPKVIYRF SAIPIKLPMFTFFTELEKKNWLA CRKLKLDFFPIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATKA/KKS FCTAKETTIRVNRQPTWEKIF AIYPSDKGLIS

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13952	44320	A	14034	707	2878	TLMQKSSIKYWNQNESSSTKSL STMIKWASSLGCKAWFNIRKSI KVIQHINRAKDKNHMIIIDAEEK AFDKIQQPFMLKTLNKLIGIDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPVSAQN LLKLIRNFSKVSQYKINVQES/Q AFLYTINRQTESQIMSALEPLTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNK/WKNIPCS GIEGRNIVKMAILPKNWKKTTT RFIWNHAKRACIAKTLISQKNKA GGITLPDFKLYYKATVTKTAW YWYQNIDIDQWNRTEPSKIIPRI YNNLIFDKPKNKKWGKYSLF NKWCLENWLAICRKLKLDPL TSYTKINSRWIKDLNVRPKTIKT LEGNLGNTIQDIGMGKDFMSKT PKAMATKAKIDKWDNLNKLKSF CTAKETTIRVNMQPTWEKIFA IYPSDKGLISRIYNELKQIYKKK TTNPPIKKWAKDMNRHFSKEDI YAAKHKMKCSSSLAIREMQI KTTMRYHLTPVRMAIHKSGNN RCWRGCGEIGTLHHCWLDCKL VQPLWKSVM*FLRNLELEIPFD PAIPLLGYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTII DWIKMMWHIYTMYYAAIKND EFVSFVGTWMKLEIIILSKLSQE
13953	44321	A	14035	869	3869	RHKKPFKKLTNPAGAEIQTIREY YKHLAYANKLENLEEMDKFLNT YTLPRLNQEEVESLNRITITGSEI EARINSLPTKKSPGPDGFTAIFY QRYKEEMVPFLKLKLFQSIKEGI LPNSFYEASIIIPKGRDRTTKKE NFRPISLMNIDAKILNKILANQI QQHIKNLIHHDQVGFIPGMQ WFNICKSVNVIQHINRTKDKNH MIFSIDAEEKAFDKFQQLFMLKT LNKLGIDGMYLKIIRAIYDKLT ANIILNGQ
13954	44322	A	14036	2	99	

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13955	44323	A	14037	1	914	TVTVIHTVARVGNLDIQQRKS ELFLSLVVCEAIKNEMNMVLMKS SPVDLVTATDQKVEKMLISSIK EKYPSHSFIGEESVAAGEKSILT DNPTWIIDPIDGTTNFVHRFPFV AVSIGFAVNKKKKVDETYLG VKETCFPLQIEFGVYVSCVEGK MYTARKKGKGAFCNGQKLQVS QQEDITKSLVLTELGSRRTPETV RMVLSNMEKLF CIPVHGJRSVG TAAVNMCVLATGAGADAYYE MGIHCWADVAGAGIIVTEAGGV LMDVTGGPFDLMSRRVIAANN RILAERIAKEIQVPLQRDDED
13956	44324	B	14038	91	1959	
13957	44325	A	14039	28	152	LPSPSSKDTDS/AASCCAPRGRA KGSVSNRSLSPFPSSVPLP
13958	44326	A	14040	35	879	GSQCSPPPASRCGSCSSAPSRH CPCRDPEPAVAGLARTPVLT TNPSPPARTGLNAPSMGTSLI/P ALCCFPLYQGSTELQCKAP**LP SPSSKDTDS/AASCCAPYFLVLL KVLSSVDNSSIWCSAGPPAQ/S SLYTIPMSSMSAKNCSVLRSGT WASFTCS*GSQRVSLGTPEALG TEDHTSRSLGHSVCHVDLSPA TASCSFQTASSEVSPATASCSF QTASSEVSPATASCSFQTASSE VSPAATASCSFTFSFFVCALWF GICPSCSAAVLST
13959	44327	A	14041	3	159	EHQCENPQ*NTGTPNPAAHQK AYPP*SSGLHPWDNRQKQPHD YLNRCRKGL
13960	44328	A	14042	54	245	GGGGGEAEDRLREPETEALSS SL/RRAPDQC/RALIMQLFQAHC FFLST/QATAALQAHYAHIFPSK
13961	44329	A	14043	903	1205	WDVSQNNKSYL*QTHSQYHTE WAKTGSIPFENWHKTGMPSLT TPIQHSVGSSGQGNQTNREP NH E*TPIHNCFKENKIPRNPYKGC EGPLQGEQLQITAQ
13962	44330	B	14044	1	339	
13963	44331	B	14045	1	1547	

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13964	44332	A	14046	807	1440	NTGKPNPAHRKAYPPRSSRLH P*DLQQTPTDLQLSDLTGPKRT NKQKGIASPSKTRISTPKPHLQ ANAQRFCFHQACVTRVPKGST KHGKEQLVPATAKTQIVKNIN AMKKLHQLTEIQTIREYHKHL YANKLKNLEEMDKFLDYTLT RLKQEEVESLNRPMGSEIEAIN SLPTKKSPGPDGFTAKFYERYK EELVSFLKLFQSEIEGILPNSF YEASHLIPKGRDTTKKENFRPI SLKNIDAKILNKILANRIRQPIEK LIHHDQVGFIPEMKGWFKCKCS INVIIHINQTNNDKNHMIISDAE KAFDKTQQPFMLKTLNKLGTIR QKKEIKGIQLGKEEVKLSLFAD DMIVYLENSIVSAQNLLKLISNF SKVSRYPKINLQKSAFLYTNNR HMESQITSELPFTIDTKRIKYLGI QFTRDVKDLFKENYKLLNEIK EDTNKWKNI PCSWIEESIS
13965	44333	A	14047	603	764	LPLFLIEYPLFLSLA*LPWPKLPT LC*IGVVREGIPVLCFCSKGMPL VFAHSV
13966	44334	A	14048	1566	1865	MQSIRKTIGIHAKYDKACRNGE DICLRETNSAADTQAKRV*SGP PANSNRPAEAGPDC*KEN*QTE RTSTPKPHLYVTIHKDQRGTQLL TNNGTKLDRE
13967	44335	B	14049	I	1932	
13968	44336	A	14050	711	1575	TRKFRNRNG*IP*HIHPKTKSGR SRIFNRPIGSEIEAIHNSLPTKKS PGPDGFTAIFYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPIGMQGWFNIRKSI NVIQHVNRTRDKNHHMIISDAE KAFDKIQQPFMLKTLNKLGDIG MYLKIIIRAMYDKPTANIILNGQ RLEAFPLKTGTGRQCPLSPLLFN IVLEVLAIRAGQEKEIKGIQLGK EEVKLSLSADDMIVYLEKPIISA QNLFLKLISNFSKVSDTKSMYKN HKHSYTPITDKQRAKS

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13969	44337	A	14051	1	1579	MQGWFNVNRKSLNIIHINRND KNHIIISDAEAFDKIQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRO GCPLPLLFNIMLEVLARAIQRE KEMKGIQLGKEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKINVQKSQAFLYIINRQTESQ IMSELRFATIATKRIKYLGIHLTR DVKDLFNENYKPLLNEIKEDTN KWKNI PCSWGTGSINIVKTAIPLK VIYRFNAIPIKLQLTFFTELEKTA LKFMWIQGYSNQNSMVLTLV IPRKMRS AVELQQTSTDQLRD LTVRKKTNRKATASTSQKH LHQNPICRSPTSKTKEVGFRSV ITNFSCLKEDVRTYHKEAKNLE NRLDEWLTRINSVEKTLNDLKE LKTMRDLHDACTSFNRRFDQ VEERVTVTEDQINEINDGNGT KLENTPDIIQENFPNLAISRPTF KFRKYREHYKDTPREEQPQDT* LSDSPRLK*RRKC*RQPERKVE LPTKGSPSD
13970	44338	A	14052	50	1105	TRKSRRNG*IPGHIYPPKTKIQE EGESLNRPIGTGSEIEAIIINLPTK KSPGPDGFTAKFYQSTNNKNH MIISDAEAKAFHKIQQPFMLKTL NKI.GIDGTYLKIIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLPFNIVLEVLARAIQREKEIN CIQLHNEEVKLSPFADDMIAYL ENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYIINRQTESQ MSELPTIATKRIKYLGIQLTRD VKYLFKENYKPLLNEIKEDTNK WKYIPCSWIGRINIVKMAILPKV IYRFNAIPIKLPMTLSSQNWKKT TLKFIWNQKRARIKSISSKKN KAGSIMLPDFKL
13971	44339	A	14053	1	764	MQGWFNVNRKSLNIIHINRND KNHIIISDAEAFDKIQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRO GCPLPLLFNIMLEVLARAIQRE KEMKGIQLGKEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKI*FPLFLIEYPSFLSLA*LPW PALPTLC

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13972	44340	A	14054	1	344	MGINQRRKAENSKNSASSPTK DCSSSPAKEQSWTENDFEELTE VGFRQQANAERFCHHQVCPKR APEESTKHGKKQ/RSISHCKNM PNCKDHRCYEETASTDLSAETQ QQKREF
13973	44341	A	14055	301	370	DDGVF*IDNHVICKQRQDFDLFS
13974	44342	A	14056	1	1418	MVREGFPPEVTFELKNELEISK GQQMGKNIPDTGASSAKALGE RELGTLDKMKNSPSDGSKKDIR THRKEAKNLEKRLDEWLTRINS VEKTLNDLMQLKTMARELHDA CTSFNSQFDQVEERINKIDVRLA RLIKKKREKNQIDAINDKGDIS TDPTEIQTITREYYKHL YANKL ENLEEMDKFLDTYTLPRLNQEE FESLNRPIIGSEIEA VSNSLPTKK SPGPDGFTAIFYQRYKEELVPF LLKLFSQIEKIGILPNAFYEASII LIPKPRDRTTKENFRPVSLMNI DAKILNKILANRIQQHIKKFIHH DQVSFIPRMQGWFNICKSINIHH HINRTNDKNHMIISIDA EKA FDR IQQPFMLNTLNKLGDGMYLKI RTIYDKPTANIHLNGQKLEAFPL KTGTRQGCLPS/ATPVQHSVGS SDQGSQARERNK GYSIRK*GSQ IVSVCR*HDCIFRKPRLSPKSP
13975	44343	A	14057	1240	1596	CYSFLFVRCPSDSQVPQLQVC/C EFAGGPLQTVFAVWSPA E VVE MFLQG*RPFYMSY/TSFEMAL MKVWTMVRTSASPVGDVFRGR GWSPFFTSTVGALT VFGVSPGS CRSSPLPSERLWV
13976	44344	A	14058	507	971	PANQKKSRTTTRIHSQILPEAQR GAGTIPSETIPINGKRGNNPKLIL *SQHHPDTKA WQRHNRKREFY TDIPDDH*CKNPQ*NTGKPNPA AHQKAYPPRSSWLHLWDARLV QRTQISKRNSSYKQNRQKQPHD YLSRCRKLGLQNSAALHAKNS
13977	44345	A	14059	561	758	
13978	44346	A	14060	2364	2663	DGQLTLVSLNHYSLAQSC EY* DGEFCFLHCSASPFL*EGAQST ACTAPCECFASDLGAV*LPQHS WCSTLLLEGAPWPGTLGTAPQF QHRKLGTLNLAG

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13979	44347	A	14061	1	64	MPIGKVGEEYIKGLTRATKESE QQSSALELSSDRVYLNEKEPGD QPWNAAFVFRGCCGVALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSLTLIIQGCKQEGFYS PSMRPRVVPKRGSA PKVRAEEN AALPSRCPPGPLPVAQP/TPPAD GGSCEQCPCSCGCCQLPPPLP WFPR*TPCDKRV
13980	44348	A	14062	1	774	MFVWSNVEGHSVAMFPWYSIP FLNPPCSHTRPSNLPTVQWPPTR ENNLPWSQLLLTSIHQAQLSA LHKEQGSSEKDGSRPNKWDK DHIRCPMSAVMIFSKRHQAL/V RAHQGHFNQDNWTVSQMLSK WWYTLGPNERQKYHELAFQAT AALQAHYVHIFPSKGRWELLH GSQRLDWGRQQLKLLGQQGQ DVLHTNLGKEENSSCWGYKME CEEFGPQGGDCGLGGVHAPL LSPEGLDSEQNTLIMDIFHCA KKLP
13981	44349	B	14063	1	753	
13982	44350	A	14064	2	1457	YPRRRPSRAGVLAGPAVLAGPP SSGRRPRRAAFPAEPFSARRS PRRAAVLAVPPSPRRRPRRAA VLAAPRVLAAPPSPRRRPRPP PSSPRRRPRRAAAGSLPGAELP QSSRLAAHLAAD*PDS*IAAGA VPRGWGLTIMAEGKEEQVTF YVDGSRQRAYAEKPPVVKTI CTV/SGHSRHNSSSGM*/SSPN SP/IPFQFTFQIPSLQAALWLCL*V TWHFFVR*PVLSSRHCFSPGGLF SLSLQSGACGPAGSLQAEFVALP PGGQSRLHRTRAS*VPGAFQEK CPLERVWPFHPSKQHPRNGLAF PLP*APQRTQPAEDTLPRHPEM GLILSQGTAG/PGRECATQLPA QHSHAEVLHFGGAMSGQLSLV GPQDSKRTARLTDSQLHLSPT* QPPGLTEGTSLEQG**S*MGWM VGVIAGAPSGWSGSGPSEGTP LFSSPA*LPWPELPTLC*IGVVR EGIPVLCQFSKGMPLPFAHSA
13983	44351	B	14065	72	1235	
13984	44352	B	14066	1	2715	

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13985	44353	A	14067	50	1304	TRKFRNG*IP*HIHPKTKSGR SRIFNRPITGSEIAIINSLPTKKS PGPDGFTAEFYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPGMQGWFNIRKSI NVIQHVNRTRDKNHMIIISDAE KAFDKIQPPMLKTLNKLIGIDG MYLKIIIRAMYDKPTANIILNGQ RLEAFPLKTGTRQGCPSPLLFN IVLEVLARAIGQEKEIKGILGK EEVKLSADDMIVYLEKPIISA QNLFKLISNFSKLSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ATKRKYLYLGILTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKCKTVGLLS NISTHKSVAHVLAEGGIPSLIN LLVCDEPEVHSRCVILYDIAQ CENKDVIAKY
13986	44354	A	14068	1	1155	MFVWRNVEGHSVAVFPWYSIP FLTTPCSHMRPSKLPVTQWPPT RENNLPSWQLLLMSVHQASL SALRKEQDSSSEKDRSPNKW DKDHIWWPMSAVIIFSKQHQA L/VRAHQGHPPNQDNRTISQMLS EQWYTLGPNEMQKYDLAFQN VEARIRY/CHRPKRARFLSHAS PPWRQLPAAGAEASGAWNLP GGG*HDYNRCSVPVFRTEVSTR PRPSEICGLTQE*TLSSAKSQVG NTFGAGHTISDTTTCGLCTSK AAIEVPEADTLPHICSWHKGEE CGLRGPEPSPPPRPSLAARVSA GRGALRRRRRPEVPPSRAPRSA ATATPANEQRAVADVGQWAR ARGGRVRAAGRSGLLRVKMM KMKTVMIHFLMKDEYIFSS
13987	44355	A	14069	1331	1584	SLQRKKAARFASSTVPRRPQGI PIHSFNVPPVGSRRLLKAPLVFIGP G*ITLNRIPYLPHSAARDPFTWN TFSFLLPCEEVPT
13988	44356	B	14070	1	1248	
13989	44357	B	14071	1	459	

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13990	44358	A	14072	1	2156	MGKKQSRKGTGNSKNQASPPPK KERSSSPAMEQSWMENDFDDL REEGFRQSNYSELKEEVRTHGK EVKNLEKKLDEWLTRITNAEKS LKDLMEKTTARELHDECTSLK RVSVTEDQMNMKREEKFREK RIKRNEQSI.QFIWDYVKRPNLH LIGVPESDRENGTKLENTLQDII QENFPNLVRQANIQIEIQRTPQ RYSSRRATPRHIIVRFTKVEMK EKMLRAAREKGRVTHKGKPIR LTADLLAETLQARREWGPIFNI LKEKNFQPRISYPAKLSFIDRST RQKVNKDTQELNSALHQADLI DIYRTLHPKSTEYTFSSAPHHTY SKIDHIVGSKALLSKCKRTEIIT NCLSDHSAIKLELRICKLTRNHS TTWKLNNLLNDYWVHNEMK AEIKMFFETNENKDKTYQNLW DTFTKTVCRGKFIALNAHKRKQE RSKIDTLTSQLKGLEKQEQTTHS KASRRQEITKIRAEKIEIETQKT LQKINESRSWFFEKINKIDRPLA RLIKNKREENQIDAIKNDKGDIT TDPTEIQTaiseyYKHLyANKL ENLEEMDKFLDTYTLPRLNQEE VESLNRPIGTGEIAIINSLPTKK SPGPDGFM/RRILPEGQGGAGTI PSETVPINRKRGNPP*/PHFM/SA SIMLIPKPGRDTTKKENFRPISL MNIDAKI/RQ*NTGKPNPAAHQ KAYPP*SSGLHPWDARIVQLTQ

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13991	44359	A	14073	3	1794	AMLPMELGCGPLPEPLPVGCSR FSLFK*QTCISTVP/GYMVTAQS MSSTPPPPSPSTLPSSPPPPPLPQ PLPPPPSPPTLSSLSSPSPPRPPL VSPSTLPSQPSSPQLLPSSSP SLSPPPPPSPLPSPPSAIPLPPP SPQPLPPPPSSPPSLPSPLPPP PLSSSPSPLSPSPPPPPSLPPS PPPSPPPPPQPPSPSSPLSSPP LSSSQPSLLPPSSLPLPSPPSPL LPLSLPLSISPP*LSLLSPLPPSPS LPSSFSQT*TIGQCFSL/VMWH VAPCTYLALAGNTLMAWPLMS ASSKASGGVSMFVWRNVEPCS VAVFSWYSVPFLTPPCSRVRPS NLPVTQWPPTRAKNLPSRQLLL TSVHQAQSLSALCKEQDSSSEK DGRSPNKWDKDHIIWPMSSGG HDLQQAAPGPGRAHQGHYPYQD NWTISQILSERWYTLGPNEMQK YHDLAFQHMAGEDIASDEEHM VIHEEEGVMSLLMTALAPLTL ISSSRIFGKVYGPPTSSSYTSD ASSSTLAPTSFLLGPGAFKAQES GEEAEDGLRELETEKALSSSL/R RALDQ/*LALIMQLFQAHCFFLS T
13992	44360	A	14074	1	2496	MLLSIDAEKAFDKIQPFMLKT LNLGHGVEQHHLHTTNDVDE EDLSDAASKGDDFALSEQSQD AHFLQPEAYGLGEGAETAATGT AHQGNHVRVEECGRSLCGCVP LVLHPLPDPSLQPEAAQGPASH SVACNQRKQPAKLPAVAHERP PGGTGSVDPRPPGATCPESPG PATPHTLGVVEPGKSSPPTMEE EPWAPQGSPCWTAQSLSALRK EQDSSSEKDGSRPNKWDKDH WWPMSALMIFSKRHQAL/V
13993	44361	A	14075	4317	5099	KMFVFLCISAQLSLQCFRGSFHF IKIYDFSQFLFLFLELPYLLLLN HFKMLELVLQQGHPNQDNWT VSQMLSKWYTLGPNERQKY HELAFQVKVAHCKND*KKFSS EAKPTSQGLAGGNKGSWEWS MSETGTATAPGVSSSELLSVAQ TLQSSDTKSSFCGAEWGHP*GI GCDDVIADDGFSTTDLDLKFKE WVTDAESGDNSGEEPEGNGKFG GKVFAPVIPSSFT/HCRPLLDPE/ PPGSPDPPAAFGKVYGPPLSSSY

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13994	44362	A	14076	1	637	MSRVGSCRWVCGLADFKNKGT DLCDKSLHNRELSAERPLNEQI AAEAEKIKKITYPPENKPGQSN YSFVDNLNLLKAITEKEKIEKER QSIRSSPLDNKLNVEKDVDFNQ EFGKLIDGYDSTKEWDVWHKF QDIPNLVGTAFNVDDGNGGF VVHWNLNKFEHFTSSTEVMFH QLRKLSDKQVDHENDADRED EEHSQEDRERGLHMKLDH
13995	44363	A	14077	448	464	KKRA*GSVSQRFPAAET*LAD*VI NTGSQEAKRREQR
13996	44364	A	14078	179	382	NTPNQRSVASNRVFKCTHQHS VKCTQSALCKMHQSAGFLKVD NHRED*KKGHSRAKTEHGRG QIRE
13997	44365	A	14079	697	1654	PKPSVGRMGFLGTGTWILVLV LPIQAFKPGVGSQDKSLH**ED LSAERPFELNRLLEAEGRTFK KTYPPENKPGQSNYSFVNDL NLLARAITEKEKIEKERQSIRSSP LDNKLNVEDVDSTKNRKLIDD YDSTKSLGDHKKFQENETADNSF SQEEEPVVAGEDLPPSPQESD VQPVQPEEVSARDFLQRLDLQI KLSTQAAKKLKESSSLERMRE ETLSPTVPTKRWDTRILLIGAF YRVLIGAFYRVLMGAFYKPIAS YRALIGVFYRALMGAFYNPLV RQKSSPRPHSTQEVQLASPLTN TQITYYVIFTV
13998	44366	A	14080	72	1117	ILENHLSDRVAEGGPLQGLRLG VQGEAVPPGLVHQRGGLGPLD GELIGSVGQQVSDVEGAGSHR G*RHTGRTPAVSAGPAA*SATH TAPMWLAGWYEPAPQPGPVLV SPPTPFQGTQASWSCA*ARCA GSWWH*HQTPGGA*RVAAAPAP SWSRSCP*RPTRSPAAAPPAPSR PGRAVGLATGAGHPAQHGHGR AVPTGPRAAGAGSWSELCPPSS CAGTSRGR*AGTRR*AAPAGSG RPGPGA WAGPRCSRSTYAAAA CGRGGA*AGADSGPRSGTHAG HCGARCRSSTPLVPAAAGHLPP PGPGRTGDPCPASSCPGGLPHG CSLSGSWGEGWVSAARQAGLP WAVA
13999	44367	A	14081	2	269	
14000	44368	A	14082	1	591	
14001	44369	A	14083	2	477	

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14002	44370	B	14084	237	419	
14003	44371	A	14085	2	1220	LPPGFVMAAAAAARNHVVWG TETGILKGVNLQRKQAAANFT GGQPRREEAVSALCWGTGGT QMLVGCADRTVKHFSTEDGIF QGSETLPGVGEGMFRGLAQT DLITCVDSGILRVWHDKDKDTS F*PTPGTESGPGVCGCAKTQA HPHVVCHRLGKRMILKIWDLQ GSGNLCFKAKNVRNDWDLR VPIWDQDIQFLPGSQKLVCTG YHQVRVYDPA*SPORRPVLETT YEEYPLTAMTLTPGNSVIVGN THGQLAEIDLRRQGRLLGCLKGL AGSVRGVAVHPSKPLT*PPVRL DRVLRHRIQNPRGLEHKVYLK VSIE/RALLLSGRDNLGG*APEP SKTQTRCP*EDTEDR*TLGDPW RQLPSGKLFVWSSPKELSKRD GERRSGLGPPADAPVPTL
14004	44372	B	14086	96	592	
14005	44373	A	14087	102	612	HCAGSPHSPRSLSGTLPGLPL WRHLRSPSAHRTCTVGAPFWAG QDRSQLP*LAGRCGGRGPGSGNP GCA/PACGPAGVPGGRGLGGPR TRSSQALPAPGNEGLSTRASG CRGRTGSPSSASPLGLSCLPAG QGWGP/GSPCVSLPPTPWAPV RPEPPG*AAPPAPRRPV
14006	44374	C	14088	1	636	
14007	44375	B	14089	31	612	
14008	44376	A	14090	234	504	SFYHLGAGE*PGKSRVPIQFQS PWGPYQCGRARGGEVCHLQAV PPRGAGAARTLSGHPLGSPEQL PQGPAAELPGGVVPRSTPPCP
14009	44377	B	14091	1	924	
14010	44378	A	14092	11	354	RLSTSPDSSGAQLASPSGSHTRA AGGAACQSAVRSP/PEPSPWV DGTGCGGAGGARWGGSGCT GAHGVGGR*PGMAG/*GPEPCP EGRQLRPLAPVGCQ*REP/G*K NSMGETTT
14011	44379	A	14093	147	513	GSASGVVRLSRWARGLAGFRS EAADLRGECYSS*GSASGVVRL SRWARGLAGRSEADLRGEC YSS*KQRGPKELRSPAGFT*WIP /LPLQLVELPASPAPCAPTPQL SG*WDIGRRGAGGGARRGSG RTGALGVGGSGMAGCRSRA LPPREGS

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14012	44380	A	14094	418	1026	WNP HQGRW SCLPVPRHALAF LSPWVIDGTGRHGAGGGALWG GSGRTGAHGVGGS*GMAGCR SRALPHGKA AKAR*EIER SASG/ TG TAGGPSTPSAATGPGAKSLI ARGQGWPAAPSAGPAKPTPT GNSSWPASAAGSSGSCSRLS/SP HLPAS*GSGLQWPWPAQKGAPTV QQQAEGLPRLPEEWISL PFLG HQGEHSGMA
14013	44381	A	14095	897	2111	PPLLQSSPNFFLICYL PWHNSHE NTHRTGRRGAGGARRGSGSR TGAHGVGGRRLRHGGLQVPSPA PWEGS*GPARNRAQRRYHCSCP GLQSGLPHYSGYHT*PDEKEKN GREGOKLER
14014	44382	A	14096	1304	1922	KL NIGVIYSSEIPDSGAQLASPS GSGTRAAGGAVCQSCALRSHSS ALGWSMG/PGRRGAGGGARW GGLQRTGAHGVGGRRLRHGGLQ VPSPAPREGS*GSVRNPAQRRW AGTAGGPSTPSAATGPGAKSLI TRGQGWPAAPSEGPAPKPTPTR NSSWPASAARS PGSRSR/RLPPH LPAS*GSGLQWPWPAHYFEFFLP GQNAQTEVSY
14015	44383	A	14097	318	533	MVCFDGA DCPWVVDGTGRRG AGGGAHRRGSGRTGAREAGGR LRHGGLQVPSPARREGS*GPAS PAGCLAHL
14016	44384	A	14098	346	957	ARYTLHIPTRLGSPAGFTQWIPH RGC RW SCLPVPRRALAFLSPW VVCSPVVDGTGRRGAGGGARR GSGRTGAHGVGGRPGMAGC RSRALPRGKA AKARREIERSAG G/TGTAAGPSTPSAAGPGAKS PFARG/LAGPAAPSARPAKPTST RNSSWPASAARSPGSRSWKMS LYMKKSASGQSAQWIAKMW KSPRFKPLWLTS
14017	44385	A	14099	124	663	SCLPVLRRLATFLSPWVVGNGTG RRGVGGGARRRGSGRTGAHGV GGRPGMAGCRSRALPRGKAA KARREIHSAGG/TG TAGGPGT PSAATGPGAKSPIAPGQQGWLA ALGINGAGERLFMKVAFSLKTC SLSCSYLRRLTL SRGGSVHVLRG NLTVCKQPQALLRVVFIHQ RQ ADCGALPVP
14018	44386	C	14100	1	672	

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14019	44387	A	14101	3	1759	RPLRGWRRTRDARAPRRRCRG SHGARRCLRKTAATSRCCGAP GP/RSRPPSTGQAAEAGDW/PAG CNP*GGLRAADGPGSRPPRGS GLLCGGGGGGSSPVVHGTG RCGAGGGAPWGGSGRTGAHG VGGRLRHGGLQVPSAPQEGS* GSARNRAQPRWAGTAGGPSTP SAATGPGRDGEGETGAHVSA LKGTPTGEWPAHGLVPYISGDQ TCLIFKVTFKAVVLKCGPQTTS STSISCPGSAN/SPSPAG*/GSSG CGSSSLCSAHSVQEDSQPQ*KR TGLQSVTYGRSGSSNEPRYHSD LPTSRSKLRNEDTFGRKKLS EVQRTGQDPA*SHHTSSYTLPG L*TAEGKDRVENAA*KGSPNFQ RSGTFNPKGGARKTRQAWHPR APNCQAGTPPREGSSGPRTSL AAFRIPQEVVNFLLISGPITRAQR HGEPESPRGQTGSPPLGKTGSE GTDKSTGADKKSTGDRQEV EPTESQGLDRKPTGMDRRSTG NRQKVRQIGSPLGLNRKPNGT DKKSTRNRQEVRRRQSAGARQ ERAGSSTFLRLSALCGLLVVDVN REQVAKQKWDLYSSRFTSGNR
14020	44388	A	14102	1879	2607	GKPSLSLHPGHKCGISRCNGNV SSRLRSPAGFTQWIPHRGCRWS CLPAPRCALALLSPVVDGTG RHGAGGGARRGGSGRTGAHG VGGRLRHGGLQVPSAPREGS* GPARNRAQRRWAGTAGGLSTP SAATGPGAKSPIARGQGWPA APS/IGPPSPPPGTAGPQAPH AAPVPAR/PLPPH.PAS*GSLQ PWPAQKGAFTVQGGG*RAPQM PPKWEPRQGRIVAFTEVGV
14021	44389	A	14103	2	272	GHWGMVNSPCRASATVSRGSP LPGVLPTSPSATSTCRMCHPR RCPLPFRRLSPPSLTPP/PGKPPL LPRPHSMPGLGLPLGGLPVFHP

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14022	44390	A	14104	101	1815	Q SARQLR PCP GAPSLAGVENRR K KTTNLTSLAAPDTQSTCGQSC GCLHSMGSSCMQHSYTYTGFLR SLWPCRCRHS AFSGQRRSEK D SKSVRERSGRSQNVPARPALTS PLTQSPGPLAPGAGSWRSRQLG TGTGV LW WQRESATGDFRTES ARSSDP SRRDWP GAKRKR EEG AATV L WACATASTAIICQDNAI SPLKSGNSPSNHLWRPQGQLPP VLGLAQPKRWRPNLTTSPSPS RMMAR PVD PQRS PDP TFRSSTR IISGKLEPMEATAHLLRKQCPSR LNSPAWEASGLHWSLDSVPG\ PCR P*GLRPSTHGAR/TFSGARP GLGGYSPPEAMPFEFDQPAQ RGCSQLLQV PDLAPGGPGAA GVPGAPPEEPQALRPAKAGSRG GYSPPPEETMPFELDGEFGDD SPP PGLSRVIAQVDGSSQFAAV AASSHQCLSIHIPMPSVGRNG LLTKPPSTSRRGKLTKRDDMY Y FV PFRSLNDMMHMLPFIEDSR WTHNLDINREQKTNP LAGPKG RPIR TQAAASTNSKTESIQIE KTEEAPFSLRYININNRSM DPLN
14023	44391	A	14105	39	877	AGPGPRPLPPRSSEGGPGASISL CSEVPGPSCQGRFRGGRDAMS MPWREER SLLAGE*PS*GG*S GRGVSRKCS*PGRGPVPRPRL RSRPRAASSELDQNSPLDQSLHR TRKTIPSSGGSTAIMPRRGSSSE TFFSAPSKTWVLGIPGETFISGP AAFPVAPGGPRAAPRFSPLNSL *SGGNGGPGPRLHFSSCGKGP PRPSNSRNGGQSACQGGSHLV C*SHRGSLGEGHAYQGDPCSPG HPAKAP SRAHAQARRSAHAAS LTSGPCDASCQAW
14024	44392	A	14106	358	546	CFPSRIRLALSRAPKWPAKRSPS EPEMS/PPVWSHPDPNNTAPPK EQPPSSPGRVGRHGNWSV
14025	44393	A	14107	22	549	DHCLCSVVRNKRDSVYPLPIPP CCKTSTISPP/LVDAVRP*DISVS KRVTSCAPLEQPHPLCLPTINAG R/TLARPQGAPT PNKEEQQAPG RATASGQAAPATTVLGDTTK/G PQGRHRTSASAA GPAPFAVA DQLPPEDRAASAEGRK*AAAFP FCHRLVQDGGPPPPAAGVPGA GES

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14026	44394	A	14108	146	2616	LAAVGMASHCFRQRRQSQSPA/ GLRGAGSAYSPA\EGARSSHGQ/ PPWRGRRRGPGDPVRGAARCR RPRAAAQPARPAARPPARPRPA P* AACCE/VPSAANSVAPSAAM *SSAGRDGASSQSRPPHAAAPP RSSALPANGK/PPSPVTRAARTC GARSSNTGA*SAARPKHSAASS RHPPPA/MPLPARHA/PGGTSG RPLTPQGSAPTSSASPRGPATP PPAGPRAPPPSPRRAAAPRPPGR QLSPAFTPAAGGGGPPFPALR *SGSVFGRQLVGDGERGRACG ARGSAAPALRTFVVSPSTVVA GAACPLAVALPAPDPLPCSE*A PLRSG*VPQASLFCQFRPQA WQHP*LLRAPCRLGAAPVCV WCHSRALDSATPRWM*G*RLP AVWL\PAFSPFFNQAFVPPCQO NCSLQNRQTLASAKIGTEEWD IAIKIPENVEVTELGNEQRLLE FGGLRRRQDEDEGKFGTPTDWL NGCDQNADSNMDSGQGEDG GCSFGGAGLRGSGWGDQRET FLALKANLRWPFRRSAQSQTSTQ EGAAGARSGLKGKKKNPLKLP KKQAKMKNKAFKQKQEKERK KHKELKAKASWKGLRPQVEFK NLAEERRGEAAVPGCPVVAGHS WRLSLARGCAKRARQLLFPSE KLLAALREGSTRGGGAASQPQ RKLRVCMRVLDSVDFHMDG
14027	44395	A	14109	1	885	MIISIDTEKALDKILHPFILKTLN KLIGDGTYLKIIRALYDKPTANI IMNEQKLEAFPLKSNTKQGCPF LPLLFNIVLEVLARA/KQEKEIK SIQIGREEVKLSLFADDMIVYLE NPIISAPNLLKLIISNFSKVSQYKI NVQKSQAFLYTSNRQTEIQMM SELPTIATKGKLYLGINHPLTRD VKDLFKENSKPL/KELEKTTLN FIWNQKRAHIAKTMLSCKNKNA GGVMLPDFKLYYKAAVTKTA WLGDDQVFLIPRGHISDYHMG KNLGQYPAFQDRGPCGFPQCIV PLVYRD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
14028	44396	A	14110	453	891	LIHLSTDALRVSGWGTVRSFSS HEAIFQTIAWGETLDNTLLSRA EVPAAAFHGALCPWFETREWQ* LLQSILLVNIWLTRHVLHSPRSL KP*FYTT*VFVCSKLGQSGWGK VAGAKLQMNINISAKQLFKVQV LFKIESLMSSLST
14029	44397	A	14111	452	2922	KMGLAREWILRFLVLILQEIRS MRQKENKDQDLNSALHQADL IDIYRTLHPKSTEYTFPSAPHC/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKLTQ/NRS ATWKLNS/YLNDYWVHNEMK AEIKMFFETNENKDTTYQNLW DTFKAVCRGKFIALNAHKRRQ ERSKIDTLMSQLKELEKQEOTH SKVSRPITG/SEIEAINSFTNPK RVPGPDGFDEPNFYQRYKQEL VPFLLKLFQSEIKDGILPN*FYE ASILIPKPGRGTTKK/EENFRPIS LMNIDAKILNKILANRIQOHKK LLHHDQVGFIPGMQGWFNICKS INVIQHINRTSDKNHTIISDAEK AFNKIQQLFMLKTLNKLGTNG MYLKIVRAIYDKPTANIILNGQ KLEAFPLKTGTROGCPLSPLLF NIVLEVLAIRQEKEIQGIQLG KEEVKLSLFADDMIVYLENPV SAQNLLKLISNFSKVSQYKINLQ KSQAFLYTNNRQTESQIMSELP FTTASKRIKYLGIQLTRDVKDLF KENYKPLLNEIKEDTNKWRNIP CSWVGRINIVKMAILPKVTYRF NAIPKLPMTFFTELEKTILKFR WNQKRAHIAKTILSQKNKAGGI RLPDFLKFYKATVTKTARYWY ENRDIQWNRTEPLEIMPHIYN HLIFDKPDKNQWGWKDSLFNK WCWENWLAICRKLKLDPLTS
14030	44398	A	14112	3	3349	

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14031	44399	A	14113	294	1107	RRHRLNYPRTAQSPHPRKAL ARSESKRDGGFKNNWSFDHEE ESEGDTDKPEGPLDAPPRP/ESG PRAPGKGL*RRSRSPGSPSERGSA ARLTAEPEARNPAASTLLRRGP SSRRARRRCGPWIKKEAAWEE EDGGRQERRLGQDLRTRTLNK SKGGIDSRJISLGQHSHPHTAKL WLDQSLREMEVLKIIGALIMKK KVKEIQIKSRARSTPLHDQIGTT SPRERTIASKRHPYITPKGIRY EQDTLSRTPIITIRSRQRLGPLT ASPPSPFTLAPPTQAIKPSLHLR EGKPTPTPGERSTRPHHPEPPRK EYALSSLYPPTYLLAPTSTDLG NAHPTQEPQFNVDATHPRQNR FIPVAGNSPKRSSQFPVFAPKK NTTPPYLDFAAILGLHRRPPRSR FRTSYPPKEFRSSPPERTAPRN
14032	44400	A	14114	2	297	VQKSVLCSFQAGTMEGVEEKK VPAVPETLKKKRRNFADAQFL QTVFLAF*YTLKGRQVYWL VEE*HQFYKISYRKKMVQRJRH PQSCTVQKSWWP
14033	44401	A	14115	3	754	GTMEGVEEKKKEVPVPETL KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRTEIRMARMARKAGNF YVPAEPKLA FVIRIRGINGVSPK VRKVLQLRLRQIFNGTFVKL NKASINMLRIVEPYIA*EYPNLK SVNELIYKHGYGKINKK*VALT DNTLIARPLGKYGITCMEDL/IH EIYTVGKCFKEANNFLWPFKLS SALSGMK/KKTTHFVEGGDGG NRVDQINTLNRRMN
14034	44402	A	14116	1	388	

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14035	44403	A	14117	1	1145	MTRNYEWLLEAESSQPPIAFQK MEPQPYNSKELNSANNQCLLE KPKLRQLKDKKEYDQGHATAVQ CQSWVYVLTDPDFCQQLILLPS TENFHECSRSDTAGHLRTGHVA SNWLSEHSPQTMPAAMQWDK KMQNTSSWFPQKAPEKVKPMS KLWQTPSQNDTLKAVKALTL SSPERNSINTNKKDVHTETSSK GHQHQRPKVDKSMKMRKNQH KKAENSQNGNASSPPRNHNSP ARERNWSENEFDELTEVVFRR WVITNSSELKEHVLTKQCEAKN LEKRLLELLTRITGLEINQAEERI SETEDQLNEIKHEDKIREKRMK RNEQILQEIWAYVKIRPKLRLIG VPENDRENGKLENTLQDTIQE NFPELAR*ANIQIQ
14036	44404	C	14118	291	551	
14037	44405	B	14119	1	1308	
14038	44406	A	14120	82	367	ITLSSPPHSFIGHKTASGPPQKI PPQPSQ/CKQWGDPTVEAC/CV SCPTQGFIPTRGPPCKHESLV VPLVGTPTRRNQPGGHIQHSQR WAPVLT
14039	44407	A	14121	999	2661	VHLTGCGGPGQPVPPEAPPRGL RSMRC/GP*GFSPGAEA*TEP/C HYGGRRFGPCGFSGLCLATNSP WLPGRPPPCSPWAGP/CGLCLP AAAAERQPALSVPGASPCRL PLVVLCHGSHLNGGRVLLRPG GSPCGHCHNCAGARRGLGHVL QGGAQARQREQLQR
14040	44408	B	14122	164	1042	
14041	44409	B	14123	320	566	
14042	44410	B	14124	1539	1674	
14043	44411	A	14125	185	780	QKAKKGKLRKSKQNSFPGLKK TVPSQLVQYCPFS*ISWKPMVY QKVPA*PRPPRTPDHHPDPGPA PHPRQHHPPPSPDAP/SPPTPT RRRPPTQPPDPHPRPPHSPKPH PPQPPPTPTATPTTEQQRHTAPP TPRPPTTHPPSTPKHHA/PHTAPP PTKNTKPTPTQRTQDKGRQKK PRRQPHHSEPNKKSPPKAHI
14044	44412	C	14126	1	1128	
14045	44413	A	14127	319	536	
14046	44414	C	14128	231	425	
14047	44415	B	14129	1	1431	
14048	44416	A	14130	75	393	
14049	44417	C	14131	174	371	

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14050	44418	A	14132	79	164	
14051	44419	A	14133	343	775	
14052	44420	A	14134	554	724	SEGPSKEPTHRRMKFSHHDDLIFLDLSN*QPPNSPEPHPPQSP*KPWPQNPSRQM
14053	44421	A	14135	20	242	VSLFMSGSGHCIRSTRGSKMVSWSVIAKIQEI*CEDEKMARES\LAESMSTYVMMNHTYDS*GKTHILIMKK
14054	44422	A	14136	229	366	
14055	44423	A	14137	131	505	
14056	44424	A	14138	1	1317	AGSCSGSRAMAEEQGRERDSVPKPSVLFLHPDLGVGGAERLVLDAALALQARGCSVKIWTATHYDPGHCFAESRELPRVCAGDWLPRGLGWGGRGAAYCAYVRMVFLALYVFLADEEFDVVCDQVSAACIPVFRLARRRKKILFYCHFADLLTKRDSFLKRLYRAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHKDPPDLVLP/SLNVTSFDFSCS*KAGMT*SPRGKNSWLLSINRYEREKGIWTLGTGKALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLSRFSQKQKISLL/RQLARVCFYTPRQ*GTLGIVPLGRPCYMAVPQFICLIRVGPFSSSI*PQCSQGFCEPDVHFSEAEKFIREPSLKATMGLGWEIPE*REKFSFGSILQEQLYRVVY
14057	44425	A	14139	1	648	MESKEEQGGVADHQKATRGIPTPQPREVVSERATQRGNRAFTKLCNPKTNRKQQQQYQQQKGRKTKLPKGQHPQRSKLDKLTEMRKHQQNTKNPKGQSPSCPPNDCNVSPARVHNWTDMEELTEVGFKKWVRKNCAELKEHVL TQCKEAKNLDKRLEELLTRKTS LERNINDLMELKT/RA*ELCKA YTSINS*IDQAEERISEFEDHLAE

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14058	44426	A	14140	1	1365	MPVKGGTKCIKYLFGFNFIW VSEDRCRALLSGPTCSRAPDTG RGRECRQLALPAPGRHRAGRES ALRLPAGSKAGSRAGRDGRDG RIRVGVSGLFGSTTGLFNQSL AETGFTPYTQKSNDFLVKS LKJ WHTYFKNFHQEARLYIRTSPGS NWNWFCFLGIESPEQPGVYEG QRPRVVTKSFASLTLKRVGTVL LLAARINADVLYVLQLAGIAVL AIGLWLRFDSTQKSIFEQETNN NNSFFYTGVIILGAGALMMLV GFLGCCGAVQESQCMLGLFFG FLLVIFAIEIAAIWGYSHKDEV IKEVQEFYKDTYNKLKTKDEPQ RETLKAIHYAVCRLGKDTLLRF LRIVSAHRLNCCGLAGGVEQFI SDICPKKDVLETFVTKSCPDAIK EVFDNKFHIIAGVGIGIAVVMPS FRSNHDPHVSSYLLIFGMIFS MILCCAIRRNREMV
14059	44427	B	14141	98	1064	
14060	44428	A	14142	560	964	KRLPRILGIRGKPCPDTSRAGR RVRGAAAAPCREAARGRGQRR FLPPTWRCETGAATMFPSPALT PTPFSVKDILNITVRPRS/LGQAA LTKRLSASLSPQSCARCRRRWS CVILSAVRGN*YAGSRAHRDCT Q
14061	44429	C	14143	189	452	
14062	44430	A	14144	1	647	

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14063	44431	A	14145	890	2905	LRLSLKFPMSPQWTPYNELYTL KVDMMKSEIPSDAPKTQESLKGIL LLHPEPIGAAKSPFAGVEMINSK VGNEFSLHLCDDSKQKEKEMNG NQEQEQESLTVVRKKRKSQQAG PSYVQNCVKENQGILGLRQHL GTPSDFDNDSSFSDDLSPSSSL HFGDSDTVTSDDEDKEVSVRHSQ TILNAKSRSHSARSHKWPRTET ESVSGLLMKRPCLHGSSLRRLP CRKRFRVKNNSQRTQKQKERIL MQRKREVLARRKYALLPSSSS SSENDLSSESSSSSTEGEEDLF VSASENHQNNPAVPSVTYQGQ WSKNIKEKTLEINSSQALTAYE CLHSAHVINLISPFYHHFPSSQE RSYLSTLSTLSNKKTGSVWFTR SPKVTQFFPGGALTGLSQRPER EILRPLALPGKGNTPPYFCSPSM GCTHCPTSPNEMNQGISDAA APVRDIYIKPPSPWDRAPGGRG GCGHSFRLKSPYLRAKSAAD FPAQHSSSDKGQAASSSGSLTP VYPVWVTPPSRGRQTPHRGEL WLASDGCPSGRKLPEEGTGSNL CCSAASAGDTQANRDHNSSPA REQTWTENKFDKLTAGLRRW VINSELKEPVLTOCKEAKNLE KRLDESPTRITSSEKNINDLMEL KNTAQELHEEHTSINSQ/DQAE*
14064	44432	A	14146	1	737	LNRGEQRAVRYYSHMKNMA EEEDYMSGFLH*CPRRYQTRIA NAKANPRSPSKREKQQEANLK NRQKSLKEEEQERRDIGLKNAL GCENKGFALLQKMGYKSGQAL GKSGKSGIGHEASLKRKAEEKL ESYRKKIHMKNQAEKAAEQF RMRLKNKQDEMKGEDLRRSQ RACQQLDVQKNIQVPREAWY WLRLSEETEDEEEKEQDEDEY KSEDLSEIKKTYLQIVQDQLLQI MTKIIPNKVET
14065	44433	A	14147	1	1860	
14066	44434	A	14148	1	1203	
14067	44435	B	14149	1	1119	
14068	44436	A	14150	1	1407	

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14069	44437	A	14151	1	1731	ERSSSPATEQSWMENDFDELRE EGFRRSNFSELKEKVRTHHKQD KNLEKRSWFFEKINKIDRPLAR LIKKKREKSQINAIKNDKGDTA DPTEIQTITTEYYKHLYANKLE NLEAMDKFLDTYTLPRINQEEV ESLNR/LNNRL*N*GNN**LTNQ K/NVQDQMD*QLNSTRGTRRS WY/RFLLLKFQSEKERILPNSFY EGIIILLIPKGRDNTKKDNFKPIS LMNMDAKILNKILANRIQQHIK KLIIHHDQVGFIPGMQGVFNICK SINVIQHINRTKDKNHMIISTDA GKAFFDKIQPFMLKTLNKLIGID GMNLKIIIRAIYDKPTANIILNRQ KLEAFPLKTGTGQCPLSPLLF NIVLEVLARAIQKEKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLSNFVSKVSGYKISVQ KSQAFLYTNNRQTESQIMSEIPF PIASKRIKYLGIQLTRDVKDLFK ENCKPLLKEIKENTKNWKNIPC SWIERINIVKMAILPKVIYSFNAI PIKHPMTFFTELEKTTTLKFIWNQ KRARITKSILRQKNKAGGITLPE FKLYYKTTVTKIAWYG
14070	44438	B	14152	1	906	
14071	44439	A	14153	3	553	EHSSSPATEQSWMENDFDELRE EGFRRSNYSELKEEVRTTHGKEV KNLEKKLDEWLTRITNAEKSLLK DLMELKTTAREICDECTSLSSR CDQLPRPDGFTAIFYERYKEEM VPFLLKLQFSIEKE/VNPP*LT/L GQHHPDTKAWQRHNKKREF*T NIPDEH*CKNPQ*NTGKPNPAA HQKAYPP
14072	44440	A	14154	1	909	MKAIEKMFFETNENKDDTTYQN LWDTFKAVCRGKFIAVNVHHR KQERSKIDTLTSQLEKEKQEQ THSKASRRQEITKIRAELEIET QNTLQKINASRSWFFERTNKID RPLARLIKKKREKNQIDAIND KGDITDPTEIQTITREYYKHLY ANKLENLEEMDKFLDTYTLPR NQEEVESLNRPTGAIEIAINSL PTKSPGPDGFTAIFYERYKEE LECSSSPAMEQSWTENDFDDL EEGFRRSNFSELKEEVQTHRKE AKNLEKRLEKWLTRITNVEKS LNYLRELKTMARELC
14073	44441	A	14155	1	969	

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14074	44442	A	14156	377	687	LLEGKLTNRKDIHTKTPSV/SP SSKTKHESSSPAMEQSWMEND FHLEEGFRRSNFSKLKEEVR THRKEVENLEKRLDEWLTRITK VEKALNDLMELKTMARE
14075	44443	A	14157	1	711	
14076	44444	A	14158	1	831	
14077	44445	A	14159	1	744	
14078	44446	B	14160	1	1479	
14079	44447	A	14161	1	810	
14080	44448	A	14162	3	651	
14081	44449	A	14163	2	1067	
14082	44450	A	14164	2	2063	
14083	44451	A	14165	1328	1639	PTNAHETSGRYIAGSSEKRTSA RTCGGTSAAARPAGTSMQTRC RQPPSS*HAVPRVAQSSDGL KATHPQAYQPCGHTPTRLPQES NCIEHERGLGKKKKKKK
14084	44452	A	14166	1	620	MTLGYGQRGANKDLRTGFDPD LCTMDNFAEGDFTVADYALLE DCPHVDDCVFAAEFMSNDYVR VTQLYCDGVNDSFLIGLLRIG CKIENERSSPAMEQSWTENDF DELREEGFRRSNYSLEKEEVR/I NGKEVRNFEKLDDEWITRITNA EKSLKDLMEKLTARELCCKC TNLSNRCDQLEERSVAMEDEM NEMKHEDKFREKE
14085	44453	A	14167	1	514	MGKKQNRKTENSKNQTSSSP KERSSSPAEEQSWMENDFDEL REEGFRRSNFSLEKEEVRTHGK EVKNLEKRLDKWLTRITNTQKS LKDLMEKLTARELHDECTSLT NQFDQLEERINNEDH*QD**R RKERRIK*MQ*KMIKGISPLIPQ KYKLPSINTINTSMQIN
14086	44454	A	14168	1	366	MDTFLQAERKDYMEAYELIEQ EEQGEREPVAVNNILSTEALMA NAKSTLMFYAVGFLWQPGGGR GHKAASNPGVTRDVGSLSSLT FLRGERSSPAMEQSWTDNDFD ELAREEGFR*SNFS
14087	44455	A	14169	1	1026	
14088	44456	A	14170	1	3906	

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14089	44457	A	14171	1643	2721	IKPTKMGKKQSRKTGNSEKQST SPPPKERSSSPAMEQSWMENDF DELTGAGFRRLVITDFSELKED VQTHHKEAKNLEKRLDKCRTN G*LEWMNG/ITRITNAEKLKDL MELKTKARELHDECTSLRSRFD QLEERVSVMEDQK\MNEMKR EGKFREKRVKRNEQSLQEIWD YVKRPNLRLIGVPESDGENGTK LENTLQDIIQENFPNLRQANV QIQEIQRTPOQYSSRRATPRHIIV RFTKVEMKEKMLRAAREKGQ VTLKGKHIRLTVDSLAEQLQAR REWGPFIINLKEKNFQPRISYPG KLSFISEGEIKYFTDKQMLRDFV TTRPALKELLKEVLNMEERNR YOQLQNHAKM
14090	44458	A	14172	351	898	SGVTPAPWRPNGLTLITAAASH PVLAIAPALHLCSPRCPFLTTVTC SGPQHHAARGRVPHF/SECCK SFRYRSDLRRHF/ARHTALKPH ACPRCG/KGFKHSFNLANHLRS HTG/ERPYRCSACPKGFRDST/G LLHHQVKTITT*PD/CGGCLVSN IVGSYSRPPWPCTRGPRRPLGSP SPAPGSVCLC
14091	44459	A	14173	1	551	
14092	44460	A	14174	3031	3207	TIHGCWWDPLSSIF*PFWGRGFI SHKICQAQISFRVISGTVLSLDK LLIMFHKAIFASP
14093	44461	A	14175	3555	3957	ENGQKTWTGTQSRRTYTGDRM AQIQNPDTKCW*ECKATGTRI CWWECKMVQPLWKS/WQFLT KLSILLPYNLAILLGNYPNALK MYAHTKGFTCMFIAASFIKAKT WKQPRRPSVGEW/INNL*LVQT MEYYSAL
14094	44462	A	14176	3	883	CQPYPRPRPTGTGHCQPPSQ GSAEP*G*CLPTLLRMALKAQP TKVNPRTLDDSDPVC/S*AAHS RVLITSPSRAPWRLPS*RRCPA GTCMPSTATSAR*CSQRPSSW *T*TGSSLSQACGPPSSSTAPPSS SWSACTCGCAAAARCSAASS TRSGPTCGSSPPASSCASSTPAP GTPSSSTLTSWASSPWSTPCPGS AGPSSWSSSSSATPSASASTRL SPGSPAAP*PWPTALSRLTEQEA VWGAWGISHGNSWDKETKLV RLPHPCSKSPCFRPSLPYRAHR AP

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14095	44463	A	14177	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL/GILLHL ESELAQTRAEQQRQAQEEYAL LNIKVKLEAEIATYRRLLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14096	44464	A	14178	2	1044	AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLRLASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALLSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNG/GGLA GMGGIQNEKETMQSLRDLAS YLDRVRGLETENWKLESQIEH LNVTRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRQA YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLSDTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV

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14097	44465	A	14179	1	2040	MPVPQLPPVSRSLAATAAASVT EPGPNEPAVRSASAEPEVKEGF PSQNHSGVHNSLIPSGGSVAPSS GRSHYGYASEDGTCSKLRVRPR LAAAPAAPFAFVADLASCCOG LSFFEGILLVRGPYRRLRATVV RDLVAVRMAEEQEFTQLCKLP AQPSHPHCVNNTYRSQAHSQA LLRGLLALRDSGILFDVVLVVE GRHIEAHRILLAASCDYFMSFT TRSTFTNYWSLGSVLATTYGA RLVSSSTARVYAGAGGSGSRISV SRSTSFQGGLESGLAAGMAG GLAGMGGIQNEKETMQSLNDR LASYLDRVRSLETENRRLESKIR EHLEKKGPQVRDWSHYFKIIED LRAQIFANTVDNARIVLQIDNA RLAADDFRVKYETELAMRQSV ENDIHGLRKVIDDTNITRLQLET EIEALK*ELLFMKKTPEEEVKG LQAQIASSGLTVEVDAPKQSD LAKIMADIRIAQYDELARKINRE ELDKYWSQQIEESTTVVTTQSA EVGAAETVLTTELRTVQVFGD STWTSMRNLKANLENLAGEV EARYALQMEQLNGILLHLESQ LGQTPRTEAQRQAQVEYEAALLN IKVKLEAEICHLTRPPSWKIGE DFNLIGDSLDERNSMQTIQKTT TRRISWIGQSGVLRPIDTKVLEA LSQAEASGTLGKQAEANKKFQS
14098	44466	A	14180	275	550	
14099	44467	B	14181	729	909	

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14100	44468	A	14182	1	1415	MGTQCDLLAKSLEDPCVDEVE DAFQGLGKDEEIEQFSDKTFG SGAIDDDWREAHECLAELVK QPVAVIEQTGNGERDEMDDL DHEENLAERLSKMVIENELEDP AIMRAVQTRPVLQPQPSLNSSI WDGS/VSSSEANPRTTACSGNAY SVCIRICFAEA/SPRVQKMIGTF LNEHYQGGQLHLSLAVLLELS P*APHLNRWLYPASPFRFCVRS LSMFGP/QMPFRYPAPYGERMS PNQLCSVPNSSLLGHPFPSPVPP VLSPLQRAQLLGGALQPGRM SPSQFARVPGFVGSPLAAMNPK SQAPMFRPDTHLHPQHRLLH QRQQQNRSQHRNLNGAGDRGS HRSSHQDHLRKDPYANLMLQ REKDWVSKIQMMQLQSTDPYL DDFYYQNYFEKLEKLSAAEEIQ GDGPKKERTKLITPQVAKLEHA YKPETIICQALCRALHINYLTKA FQQAFEVSASITTYR
14101	44469	A	14183	204	560	QGYWRGCTSSGGDGGCRGCW SPGKRR*GLSRTASGPPAAVAS PGRPRSPPSARTG*S*PGA*ARP CSRTW/PPRCPLRPSSAARASA SRV/APL/GEPAPANTNIYCAAL THRATKSSTREF

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14102	44470	A	14184	59	1695	DMPWWVPVLPWIKDSSPSSLEM NPDNTSGLRQKSVEAEPCLW MVHRYTPQSTGEACTMAKAA GPSSPGSCPPRLGADPWPMR LSH*EC*KTGTTASGYRRHQET APPSSGSPVGLSAGLWLSWA WPVSPACLHPGPPLCP/GPPALG LGPRSPAAS/C/PPLPEAPPACSP FCP*GEISSSGPLEVPVQV*LPGD LSEPLGTSTPLGRAPGLCSLLRA P/RPGAACPPASPSRPAMLLS*E APRRPGPSGETSPSPSLAPSEASP G/PPRHNGRDSEGAGTRTFGA SGSSKG/LGGQPAHPGPGGR*G GGRYRGSAAGSVHSAAPGCGSP HAPGCA/CDVRG/AKPSHFHSG CQSG*GHQTSGGCPHLGLSPCS TCLCAGQLQQQK/PGSSGNL* GQGHSGLDLSAPPHLVPG/PG PLTAGGHG/SLVGDSEWGSPAP GAVLGQNSSGPDQQRAGR/WLC SRAEKSGCYTAPPLG*LSAQFQ EEKASWVPVPGSGQLEDSDHPDPY TALPLAAPPWGTGTGCPPAWP RL/EPDDCGPRHLSPTCSTLPS WGGCAGS
14103	44471	A	14185	264	643	RCLRPGEGRSRQGRSRTGRGK AEEGGARTQQRRAALLPERS ASQPGPRDSPRWRRRQTTRGR ARPASSGGT*GSSWLTLAWPPR EP*RLRSASAQG/CRRQRLQQR RRGLYQPHRPATCGPRAAD
14104	44472	A	14186	114	1039	QSQRRLPLADTPRRSNRPCSAA GLLFPQSFWSQELSQAFLPPS SPCLHCLPGTAAASRIHQRSPT RPSVQERRETHGLCAHRCWE AGSPAHP*AHRFVSRAGSPA GP*AHRCISRAGTPARGPYRR* VSEAGSPA/AVVSAPCSLSS*AC VTG/CSPAHS*AHRCASRAASP EHTSREDAEQAP*MQGLCPVH QEQQPSRKSVVTSPIHPETDCR LLPKNPCANKHQPTATGGRAV PPEVQHVPPRSGMTLGLSHQPLA LQFQMQATDAARLGLSPOGQG SPPGPRSTLLGLCLSLFQLSLLR

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14105	44473	A	14187	1	1629	MIIVYVENPKQSTKCVRAYTFS KVAGHKAIEKRLEKLAVDPHR DRAQMLKVENVQQAQQWIN KLPPARREDEDVKEIRWMIEEL RVSFYAQQQLDHTGVDRGQPGA STWSASLMCSVTQPKLKRKP GFLGLGERNCFSVYGAGRSW GRGLGSCGFWLPPRTRIRAADV CLARWGWRAHRVRVLAGKNS RAESMLWSFHKAIEAARTNI QAQTRVEAAQATERRIAADIDD SELKAPRDGRVQYRVAKPGEV LAAGGRVLNMVDLSVYMTFF LPTEQAGTLKLGGEARLILDA PDLRIPATISFVASVAQFTPKTV ETSDERLKLMFRVKARIPPELL QQHLEYVKTGLPGVAWSFLYSI NQTICLRLDSEIAKLQALEATC KSLEEKLDLVTNQHSPIQVPM VAGSPLRTTQMCNKVR/CVNP* ATVVPVPVPPPTTQQYQGLDA GATTRVPRSLRSEGQSTQKSP SCGSHSQDNSGGRKAVGARRD RWWLGAGKGPDCRGAKCGLP LSGQKCPDLPYQVVGCTSKTG
14106	44474	A	14188	3	1010	GLQTQLVPLSSPVASLDNFSNL FGADLHVEKGQVPSSDQHL RCHFPKAPPWSVCKALLPRSNP ATLSGTSKPNSSGDFNSVTKS QPHCELNSFVLTHGSPVLWMM SEHDLADVVQIAVEDLSPDHP VQSCGTVVVLENHVVTDDEP ALKRQRLEINCQDPSIKSFLYSI NQTICLRLDSEIAKLQALEATC KSLEEKLDLVTNQHSPIQVPM VAGSPLGATQTCNKVRCVVPQ TTVILNDRQN/DHCSQDGRPL EQQGTGFPKMSLASQ*HGTNP TFPCHCAESHENKSTLSQGT QHTLHLCGHRVPEGRHRPSSLR SGRAGWAMLNA
14107	44475	A	14189	1	1710	
14108	44476	A	14190	52	457	
14109	44477	C	14191	1	838	
14110	44478	A	14192	92	514	
14111	44479	B	14193	1	531	
14112	44480	A	14194	1628	2008	

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14113	44481	A	14195	2	1616	CPPRRRPRPRAPPHRRPPAAGA RTAAAGDRSRHGPASRVGTGP GQQMRKTYCRNSEPSDLLDQGG GSRGGPRRQSKCVRNWWVLGL TDFKNEAADPHDSGAQLASPSG FRTRAAGGAACQSRAMRYS A1.GWSMGLGAVEQGVV1.VGE AQAAQEPMEWVGSGSMVGCR SRAPPAGRQLRPDKKLSTAPVG RHRWRPSTPSAATGLGAKSLIA RGQQGRLAAPNKTDFKARAVK KDKEGHYIMIKGLVQKESITHNI YAPNTGAPKFTKQLPLDLRNKT DSNTHVGYFSTPLTALNRSSRQ KVNKETMDLNYTLEQMDLTDI YRTFYPTTAEIFYSSEHGTF TDRMIGHKTSLNKFKKIEIIPSTL PDHSGIKLEINSKKNLQNTNT WKLNNLLSDHWVNNIEKMEI LKFFKPNDSDDTYQNLWDTA KAVLTGKFIALNAYIKKSERAQ VDNLRSHLKELEK*EQTQPKPS RRKEIMKIRAELEIKT/QKIQKI NKSQSWFCEKINKIGRPLARLS KKGREKIQISSIRKK
14114	44482	A	14196	1097	1686	APRPLALRFGPLPSNSGAQLASP SGSCTGLQVELPANSCTVRWQ VSALGWSMGP/GPGAGGSAD QGGSGGTGAHGGVGRFRHGG AAGPEPCPMGEVAKAPARNRA QRQWAGTAGGPCASS/NSC*PG C*APYCPGWGQPAAPSAGPP SPRPRTTRAGPQAPWAAVPVPAH ASP ¹ PHLPAS*GSPLRPGQSGKT YQKSH
14115	44483	A	14197	647	1496	FLNLLSQWNLMLCGLKKRRKQ FKDYEKKVKELNEERDKYRKQ SVYIYTFGKEPTLNKVLDAACDG KFQAIDFITPGTYFMGCRWSC LPVLHCALAGLSPWVVDGTRR PGAVGSAGRGGSGGTGAHGGV GRFRHGGQLQVRSPAHEVLRLPS EKSSAAQWAGTAGGPCASSTA ADLGAKPLTARGGGPAGPPSA GPPSPRPRTTRAGP/PSTVGSPP/ SPPTPLPPLPAS*GSP ¹ SGLGQP RKGLPQCSGGLKGWLLKHRQS GCPGRGGAQSERGLRGLPARC

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14116	44484	A	14198	1	560	MAALLLVGASWL/LLLLVGASWLLARVLAW/TYAFYDNCNRLQCFQQ/PPKRNCF*GHLSLCGA/TEEDMRLMEDL/VPLFRDVQLWWLGSFYVVL/SLVHPTFTAPVLQASGG*PGFTTTMGLSFKRAKWQRLA/SEGSVRLMEFHEISLMTLDSLQKCIFSDSHCQMVSPGSCTTSRGPRI GALPTGGARAPE NGDPKEIE
14117	44485	A	14199	175	2225	RWSSVSFASGMPSPAPCCWGHPQCPSAAQPTGSPWAGCRGLTM PNGQASPAS*VPPGAFPLCIKQPLWENLMTGVGKFSREAA TLE GPTLPTTR/GVGPQCRQIADLPLE RTEGWRGDIGNPVRGVQRKRLQVAGETAASLLPCQASGESCSVP*QARGPPVLFLPQ/WGRRWA KGCASRSCF*PDRPSHAPGA REGAGLAAAPKRVARLSPAVPP ACCGLQGSSSAAQAL*PQLS GPRLPREK*GA/PCWRRGGPRCC PQNSAPETLEYVEPRGTGAPGT THTGLPSPSQGCRGAEGW/WGL PGLPGPRAGSSPQPRGAWRPR ARTPPASWAAKGRGRPLAAG GLARPRDPGPGSGVAPAGSLRP HSSGRGWGRRRLRARPTGGNR GSEWPR/RPPGYPGARPGAPSVR PQP/PAA*TRPLPVCGGARPFH PVPATV/VPHAGPP/SGMGRRRG RYRPPASARPAAGCGAGSAEPG RGTDKGGDGGEGKTKRGGG/L GGGAGAPKAAPGAAPMGGR GAGAGGGGA/R*GGGGGGSG TTSGSSSRPRPRTRAPPETDP APRPRPGLVRAAGGGAASGSG TGRGAEGCGVRAARGVPASLR AALARGAQARVLVSGPAPGWA EPRPAGGARGVGVWGPVLGAP GRGPRGGAGRGPRALSRGCAA *AWTPRGAGQGRGPSSRGSG

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14118	44486	A	14200	1	2850	MHPQERTAAATNAAIIITDGAA TQMGVSTSPAGHPRDGYQQG KDVSLLAHTHSFKISAAIEAKTT WVGMCRWGCKVALDVTDFVH QKGPEGAGRNKQIPFIQDFPFAL RSEKRPSLPATISGKTLPLNTKT CPQLLQCKREGHSLQCLIWLQ MVPQLGRLAVGGCHSNWFPSP KKAVIWEKFKHNLSGLVSDKG GKRTGKGLGECLLMMRKMS ALEALTTFDSSLQHHPRTTFVPS ALEALNPGKPRQLVTPA
14119	44487	A	14201	1	1570	MQSATSDAGSAPKKQKKVMTL QEKSGLAWYFFTAQWPNTPP KLRTCTESMGCLLDCCCTGQ GDWTRVTLYCRYPFILFGTNA WVANFERPRMNANSLASPTG LSPYLRFGLSCRLFYFKLTDL YKKTTLGSLPDAAMAFVNCHG AGGTVAVRTSRGHSRCHFQFG VSGTRYHLLTPQVVWERQQQK VDSLLGTQQMLEAQGREF/PGP CIPLPVPTNAPAAKTTQPPSPD L*PPNYLFLCVDGHRPIC*EPKQ NKSDSFTSQA*SQDG*YCGCS/C RAPRPHGTSATIPMSSSCKRFQ SSPF/CKGPYHFRFLEERPLASRP SIHPSGGSYWLRLGCVAVGRTG /SRLNLQLHSASGLQALSKQR*R YCQSAGAGSPEPPRGGTR*CCR EAAAPGCRAGTSPSPAANLPSLR RK/PGTC*PQNPPGRGCGSGASA AVLAETPARIKRSFPRQSCPR TWMAAGAPGSSRRQGTKHVT* *SSTLEKQLDNPTATYFVSVPTRK PVH*NQQKDL*VTG*LQIFHL
14120	44488	A	14202	11	356	VSGPPR*APWCPLAAPTGSTS HGSTARDSSTACKVS/GGATCV/ SGCGPGLGVLGRGLSSTRSCCM PAG*CPSSKDTCEKSGGRTPV PPFEWAAQDASLVRRCRILAH PCRGT
14121	44489	C	14204	333	473	

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14122	44490	A	14205	344	1035	QSAAQWFWWPGRSASLGGA GMQPPLASWPHPRISIRCLR AP*QFTNATDPRFRSAPRRSGQ QQPRGSSGPAALASPSRQPNR AGALRTGGAGWATALDTWSC PRTRRRAPMGSL*AAAQQCV TGATWPPSAIA*QSAAQWFW WPGRSASLGGAAGMGPPLAS WPHPRISIRCLRAPAPCSGPSASS AAVQVACCCSLACCGPSRPASQ GHLDGTPHTSPETCTTSLWSPQR RRAAGPPKVVDIPD*RGSRRLPS GRGAPNTTCIPYGGSPGAKWIE GCPAQ/RPSPPLHPAMRASAL LLMPFLQRRHRSAIRLLRPGS DCTGKK/GKGLAGPETKRQKR LCPSPKTLGRALGQOEALPANV RC
14123	44491	A	14206	41	292	
14124	44492	C	14207	480	1637	
14125	44493	A	14208	3	410	SPPCGAPPPVFCAPAPRAPAPP RAPPLAEALPGFASAAAGSAPA RSGPAGAG*GSRSRPRARASAS LAPASAGDHLGYPSATAAAAP ASRPWLWRPSLNAARLGDPA GWQASQWAAGSA*RAGSQWA AGEARA
14126	44494	A	14209	1	1274	FFFFHPLRSLLDGLHQSERSA PEIKPGALESTWSQARGAALRL AEAR*RAAPAAGTACSAGGAA SSPR*GSRATRRRRRGPTAPSR ATAPGRGAAASAAPARPART ALMASARGPP/TAASPAQALTR SAPGHLPPMSELGAVTALCESC PVT/AAPRSGGGEAGGTASEW GRTCRNYG/PAPGIWRPPLSAA RPAAASPPARRIWSPPAPVHSA ASPIGLRVAAPCSSGSAVPLRSR RASPPCGAPPPVFCAPAAPAP APPRAPPLAEALPGFASAAAC RGKRLRALQGGGLGRSGSRQ GPAAGS*LRGKSWSPPPGSA PLPLAQVLQALVEAGSRSPRA RASASLAPASAGDHLGYPSATA AAAPASRPWLWRPSLNAARLG DPACGWQASQWAAGSA*RAGS QWAAAGEARG
14127	44495	A	14210	2	335	

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14128	44496	A	14211	344	1062	TRAEVTQQLSRFASPPVLRLL RSYVSPPAAPTADPRWRPSWST SLRWVVKPNVSAAYRIPPRASNR GYRASDWKLDYA*WTGRLRIT SKGKTAYIKLEDKVSSELFAQA PVEQYPGIAVETVTDSSRYFVIL RISDGTGRSAFIGIGFTDRGDAF DFNVSLQDHFKVWKQSEISKE SQEMDARPKLDLGFKEGQTIKL CIGLCSKPGTTAIQLGPVLNGIG RTLRTDLRNKNDLEGTNL
14129	44497	A	14212	573	1017	TDQGVGSPICPRFQCGPPRSPR FQQRSPHSPDSSRG/PPHSPRFQ QGSHPHTPDSSSG/PPYSPDYSSG HPTP/HTSQQGI PC* DGHGWLPC GPVFLWSEAPHLNPLGLVWGQ PRAPALPGNSAESKLVPHDRPA RPETPGAGTAWAHQALRV
14130	44498	A	14213	707	836	
14131	44499	A	14214	724	927	SFMDFRFVLLFFHLVNPKN*RP VS/SPPGSKLLVPPWGPKT/PPVP HPSPPPPAHGEPGLPPPPPPPLPH
14132	44500	A	14215	29	157	
14133	44501	A	14216	1	363	
14134	44502	A	14217	770	952	
14135	44503	A	14218	1053	1995	KSSPEPDLSHSFICSPNFPSSSL KRPH/FQSSILACVFCITADSSRA PCVLRVCDGFAGLTRSSAPSSK EKPCGFSLPEFTPLAVSFPQAAL CSLGTVSCLRPRPOLTPSWECP VLLAGAVCPGLPCAAGCPWA GEEGCPGATSQLDQVSWPSLQE APEVLWPCLDSWGWFAPSTV IPLMASPRFGFMGRSQQPVLIN HLIKEPKAKFSKNHNSIRCCQG QRKWRRGNAAGMCCQPQIPGK GEVKTEFQPVSNRNVNYGCTM HFQETLWTPRLGLGDGDSNNN NNNNNNNNITANPGKEAEKPE HPHLLVKM
14136	44504	A	14219	482	833	THQGARGCTHARVSVREMRTR RGRWATGMVRPAPCSSVHTTA VQRQQVADQLQTTAELSME/L N/KWDQDPEAFVRKVATSYET WIS*YYPEDKAQSKQWLPRSGS GATLYSATNQYP
14137	44505	A	14220	195	367	

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14138	44506	A	14221	989	2210	LLVSCAILLSVSLHSSSFVRSRS NRDSPACVDATYRGCSQCGEG VCGEACSCFPDLNPQGVHAG EGVLPCSGWEDTFGKNTCLVS YQQIPNRRRPCTCECGKAFGQ RSHLVQHTSEKLYACQECGCTF SNNSSLVKHWHVHTGEKPYMC GHCCKCFRESSSLAKHQRVHT GEKPYVC/GESTHLVQHW*FHT GEKPFAC/HR/CSKAFADFSALL ACHGTYTGERPYECRVCKAFS PSLSLAEHIRCHTGEKLYACQE CGKAFSHSSSLSKHQVHTECG KAFSQGSYLQHLKIHSGEKPYI RGEHPYACGKCGKTFHSKFLT QHEQVRMGKPFMCGDCGRAF MQTSSLALHQRTNNGEKPYKW NECGKSCIQMSHLTEYYQNLPE KGSKDPHTDATVHSPVMD
14139	44507	A	14222	1	245	PPFRKQQAQHRNKTVLVRSQP VPVTVPE/PSA*RTPEGPRRAG CDPRP*PCPAGPELPAQMKVLA IEQLLSLHFKKALLF
14140	44508	A	14223	477	947	LCSSLSPPPPPPPPPPPPPPP PPPPSPVPLPPSPRPVSPPPPH SFQGRSPPELGSSAEPWLRPGT WV*/PPPLTFSQEEAASSAQK*N CPGESVPQVPVTVPERQPDAA NHSLLLPGQCFWCQGPHPY WMGPVDASSGFLSQSFY
14141	44509	B	14224	438	1437	

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14142	44510	A	14225	584	2866	WHFAKLSRNTQDHTRP TLGAA QAVPATGQPAAPG PAGAGPEW VPFLAVYKEQLVRNDSVLKVFF FPPIFYREGWVCCSVVESH LQE GFVWLFSLQL*PPKLRSLFSLSY CLSPSDIEISRQGT PKAVDVL A KEIGLLADEIEIYGKILVSSAGF A*VVWEIL*NSLSPPELRITPTPL GEGKSTVTIGLVQAVSLGLCP S WQLYLVT PALPGQQSETLFLK INK*KDILFL*FNLHLTGDIHVVI SCELSKFM DN*LLCGLIFVLCFF RGILVTLCLFL LKLLTFFLLNH *KLGIN KTDPIRTMPDTHQVAG PYLSTDD*SVLFQ*SPAPCGNG HPTGTVADHYLCLGW/YQAQF DIAVASEIMAVLAL TDSL GREV PRG*PLPG*YFVRNLMFFSHLPQ IDLGFHASVCL LGF*FAFSL*G TPVFVHAGPFAADRDLC PYQFL LCQTHIYKIHVIMAEYFQRYKL MMYAKQTSPLCDLEQAISL SGC VPCRHS HLKNEKFSCTGC*QYL PKLSLPNSDPLTLPFSADYGFKF ESNHANHS GDCQNLPLFLEDNS TYSTCFPTVTEAGFGADIGMEK FFNIKCRDVLSFRSVV*AFLLL AV*LGRFGGRQYTG VVWLLFS FLQNIQLVADGV*MVSLSKT* LNGYRCKTTNIFFTRTDTRAEID LVCELAKRAGAFDAVPCYHWS VGGKGSVDLARAVREAA SKRS
14143	44511	A	14226	3	587	YPASAGLMLQNFGVIGLRYHF AIHSPAAGGLDGLHA VAAIQG ITKIETTPNHQRA PAHWTLTQ QAHLQPSPLHFNLP LTLCLMHC PTAIPHCFA DARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEGDFQPFTRVT VHWGKG NDQTFRGLLDTGSEL TLIPGDP KHHYGPVKVGAYGAQLL

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14144	44512	A	14227	2	1256	CHCGPP/VKVEAYGSQVLKGVLAQVQLTVGPVGRPTHVPVIFPVPECIIGIDMLSSRQNPHTGSLTGRVWTIMVRKAKWKPLELPLRKIVNQKQYHIPEGIVEISATIKDLKDAGVVIPTTSPFNSPIWVPVQKTDGSRWMTVGYCKLNQVVTPIAAAVPDVVSLLEQINTPPGTWYAAIDLANDFFPIPVHKAHQKQFAFRWQGRQYTFVLPQGRWEINMTKIQGPSTSVKFLGVQWCGACQDIPSKVKDKLLHLVPPTTKK/EAQCLSGFRREIHIPHL/PIYRVSRKAANFEWSPEKEKALQVQVAAVQAAWPLGPYDPADPMVLEVSVADRDAWSCWQASI/GHKVGHAQQHSIIKWKWYIRDWARADPEGTTKGGQRRWWQLAEHQDSRDREAAIGERQETA VGKTDARDEAVCD
14145	44513	A	14228	155	531	GNLWSVDLRFPGTPLRQNFRTIRQHQSRFTKNHCSQTPLLIPIRQTGSGVDLSKLQQTCS*GSCLVCTIDLANAFFSIPVHKA/HQKQFAFSWQ/YTFTVLPRLTWLQPC*VPNLPAAETNTEPSNGT
14146	44514	A	14229	1	518	MTVDYCKLNQVVIPIAAAVSDVVSLLEQINTSPGTWYAAIDLANAFFSIPVHKAQQKQFAFSWQGGQYTFVLPQWYINSPALCHNLIRRDLDLDCFSLPLDITLVHYIDDLMLIGSTIKWVVHSS/DSIIKWKWYVHDWARAGPEGTTNGLAG*SGTCKKHEWKTGDKGIRGRG
14147	44515	A	14230	281	1140	VRVLSPEKEKELKWKNTHTKLLSYPTVGAATQLNLAMGVI GSHGARGQVVALNRQQRQGDLPFTRTVTVHWGKG/NMQIFGGLLDTGSELTLIPGDPKHHCQPPVKVGA YGGQVINGVLAQVQITVGPQTHPVVISPVPECIIGIDILSSWQNPHTGSLTGIMVGKAKWKQLELPLPRKIVNQKPYCIPGGTVEISATIKDLKDAGVVIPTTSLFNSPIWVPVQKTDGSRWMTVGYRRLNQVVTPIAAAVPDVVSLLEQINTSPGTWYAAIDMANAFFSIPVH
14148	44516	B	14231	1	1521	
14149	44517	A	14232	3	202	
14150	44518	A	14233	2	367	

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14151	44519	A	14234	1	553	MTVDYCKLNQVVIPIAAVSD VVSLLSEQINTSPGTWYAAIDLA NAFFSIPVHKAAQQKQFAFSWQG QQYTFTVLQPWYINSPALCHNL IRRDLDCFSLPLDITLVHYIDDI MLIGPRQLLACY/WALVETEHL TISHQVTMRPELPMNWVLFDP SSHKVGCAQQHSIIKWKWYVH DWARAGPEGT
14152	44520	A	14235	3	728	
14153	44521	A	14236	1	635	
14154	44522	A	14237	3	266	
14155	44523	A	14238	1	1245	
14156	44524	A	14239	2	837	CHCGPP/VKVEAYGSQVLKGV LAQVQLTVGPVGRPTHVPVIFPV PECIIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSRMTVG YCKLNQVVTPI AAAVPDVVSLLSEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPGQRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPPTTK K/EAQCLSGFRREHIIPLH
14157	44525	A	14240	1	533	
14158	44526	A	14241	1	1043	MTVDYHKLNQVVTPIAAAVPD VVSFIEQINTSPGIWYAAIDLAN VFFSIPVHKAAHQKQSVFCWQG QEYTFTVLQPVHINCPALCHNPI LRDFDHFSLPDITLVHYIDDI LIGPV*NMMLHLVPPPTTKKETQ HLEVLFGFWRQHIIPLATPSSP NGPMNKVTMMA/ANVG YAWD QKHGLPLTKANLVMAIGECV/ SPAAETNTPEIWHSSGQDSQ VQESKGGNGSGTTHHH**STS KIFASCSDITFCWPRGLSSRGR NAATRRHNNNFIIKPEVKIAFWT LWDPPTFKSTG*ERS*SVGW D*HELPR*NQSTTPQGSVSIIPH GQPPHQLFGVAKARTFGIT
14159	44527	A	14242	1	336	
14160	44528	A	14243	3	1885	
14161	44529	B	14244	1	1423	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14162	44530	A	14245	I	1361	MIISIDA EKAFDKIQPFMLKTL SKLEETASPSPVVATVYTPQPM PSAFPPLSEENPVL PETTVMAS PEAVTRQDNVDSPQKPPPTPMF ASRPITRLKPRRAPSEEGIQRLLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAAI.NHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGKAKWKPLEQPP PRKIVIQKYHIPGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSRWMTVNYHKLNVET PIAAAPDVPVSLLEQINTSPGT WYAAIDL.VNVFFSIPVYKAHQK QFAFSWQGGQYTFITLPQGYIN SPDITLVHYIDIMLIGSSEQEV ANTLDLLPARVASWGVYPDQL T/GGRED*GLLHRWSCRICRHH PQGSWQES
14163	44531	A	14246	I	1795	MRKCGKPFKLQGTNKANSRI QEELIHSKSLIEQEGEKPVQFSA FHRMWQPADSQCDIIDSADIWA DPLVRHREITGSGGINRRRTRG GRGRGGEAAGGAENCGSREER ERAGVGTAVTQLQN.LNTIGIIGS RGGRGQVAANHQRGQGHSHYC KGQKQNSNQNSVTHVELWHI WLNHNSVPRSEIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGK RNDQTFQGLLDGSELMILIFED TKHHCGPPVKVEAYGGQVING VLAQIQLTVGPVSGTHPVIY PVPECIIGIGILSSWQNP HIGSLT SRKTDGSRWMTVHYHKLNMQ VTPIAAAPDVPVSLLEQVNTSPG SWYAAIDL.ANAFFIPVHKAHQ KQFAFSWQGGQYTFITVLPQGE TLVNFSLPDITLPHYIDIMQI GSSDQEVANTLDLLPRKSTTPS G/LYGFWRQHS/HLGILLTPY* VTQKAA/SFEWGLEQEKALQQ VQATVQASLPGVYDPADPMV IEM/SLDSPSHKVGCAQQHSII KWKRYVCDQA*ASPEGTS*LY CTSFIMEKEEVC/L.SLEQTL.TLD MGLPILHAMLWHLWIHGLPY PSSWYSTQOCL

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14164	44532	A	14247	55	1241	NRFVRAAPASLKRSAGIGLLCM PDLTVGIVVTQLKLNAMGITG SELTLLIPGDPK*HFGPPVKVGAF GGEIVNKYLAQLGLTDDPVGPR THPVAIFVPPECIIIGIDILSSLQNP HIGSLTRVRIMKKGAIMKGY YEGKGKAKWKILELPLPRKIIN QKQYRIPGGIVEMSATIEELKY AGVVIPIPTTFPLNSPIWPVRKT DGCWRMTVDYCELNQVVVPT AATVPDVVSLEQINTSPGTWY ADIDLANA VFSIPVHKAHQKF AFSWQQQQYTFVLPQGWTV NSPALGHNLIQRDLDRFSFPRDI TLLVHYVDDIMLIGSSEQEVAN ALDLLVFSDDLAIKWMHSSIA SSSGSGICVIRLKKVLKAQPAP MASWGVLYDQLTEEEKIRA
14165	44533	B	14248	1	346	
14166	44534	A	14249	485	717	
14167	44535	A	14250	1	345	
14168	44536	A	14251	300	689	TKRAPCSPAAGSRGRARSLALL TLVYHGHYPALPPGPTPAQQPGR GLAEAAEPRGSEGGNGSNPCG RA*DGSRREGRGRLGGWRPC CEPQPWRQAHPAGPDRVDGG ERRAGVLRGQDQDEKKKPK

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14169	44537	A	14252	1	2430	MAVLQPSRHRLRPQLGLEPDN WHSQQDEVSVA TARAVVPSG RGAAWMGPGSNGGSLVSHE CGEGTGAAGSTQLQEGMHFCR QSRWAFLTALCEVYTQSLQDT VQWLQLCQWSAQGGDDHTLIE WLMGATWTVVNDAREIPETG TGQDAWLCGWSGVDDQRPVH ELAIHCSPNTVQRVLALVDTGA DCSLVFGNPVRKPDGTWQMTV DDWELNKVTPPLHAAVPSIMD LTDHLTLMELGQYHFVDYVHSP TICRGLVAMELAAWKCKPGVL LFHYIDDIMLTSDSLADLKVAV PLLWQHAAACGWAINKSKVQ WPGLSAKFLGVWLSKTKAIP AIEKIQA YPRPTTMKQLQTFVG LLEYWRPFVPHLAQMIKPLYGL SKKGATWDWDNEAGTDLAA KWAIQQTQALQVIDQGCPFELD VHVTTDGGFWVLWQRMCEFR TPVGFWSQLWKGAEQLQYSLQ KELAAAY AALQAYETVTDWA TVIVQMSYPIVGTGTATQTTL AKRGAYLEQQSMLTTPLAAE LQEALGPVLMEDKAMGPEAPL DPEPSLLKKGYPLVPDGAWYT DGSSQGA AAAWTA VAIQPI/TD TI*FDTGCGQSTQWAE LR VVE MDILEACQKCPACAQAYLRQR QLPNVTQQVTVGQMP LTRWQI DYAEPLPKLQGYTYALMAADI
14170	44538	A	14253	2	239	
14171	44539	A	14254	3	211	VVYYSPNEVKVVAEGFDSANG INISPD KYGL* NIFILQLWC WPNSLLCFLCQCENSFLDIYGIL
14172	44540	B	14255	13	87	
14173	44541	A	14256	42	854	VLVFLTAALFILPTFSNSMMILQ VSGGPWT/VILRRGVLLGVAPP PSLPAL/PENSVYQERQECYAFN GTQRVVDGLIYNREEYVHFDS AVGEFLAVMELGRPIGEYFNSQ KDFMERK RADQLPDCRDPLMP D*GVWISPLGQV PNLTAQKTL QHLP SKKEPQQHDDL VYHVT DFYPDSIQVRCFLNGQEETAGV VSTNLIRNGDWTQFLEMLEMT PQQDRT*AGVQLLEVTLNLSLF FLEAQSDSVQSKMLTGARGLFI NYLQLNLCTP

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14174	44542	A	14257	3	571	QGRATPENYLFQGRQEYAFN GTQRFLERYIYNREEFARFSD VGEFRAVTELGRPAAEYVNSQ KDILEEKRAVPRMCRHNYEL GGPMTLQRRVQPRVNVSPSKK GPLQHNNLLVCHVTDFYPGSIQ VRWFLNGQEETAGVVSNTNLIL NGDWTFQIVVMLEMTPO/QGE DVYTCCQVEHTSLDSPVTEW
14175	44543	A	14258	1	1677	
14176	44544	A	14259	2	430	
14177	44545	A	14260	821	1428	QVTDVQDFPLKCKIQWRRTVR GDLQ/PFTRVTVHWGKGNQDT FQGLDGTSELTLIPGDPKRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQNSHIGSLTGRVRA TMVGAKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT GVIPTSPFNPSI*PMQKTDGSW RMTVDYL
14178	44546	A	14261	507	910	
14179	44547	A	14262	1	2898	
14180	44548	A	14263	1	2580	
14181	44549	B	14264	159	2657	
14182	44550	A	14265	142	377	NHLLRRQQWQTPPPPSWS/SPR SSSDCCGSSENFKPVDSLGLSV GVGPTEPDHLDPLWLPFPQSGE RFCLAGVPGATG
14183	44551	A	14266	363	638	EVVKESGWHLAGAPLGQSFG RKEQAVIFAVLQPLLVIKQTGS GVDLQQTPAHLQQRGLSGCLQ SLCSLTSS*PQRHPQNSSLVNSC VVS
14184	44552	B	14267	1	2424	
14185	44553	B	14268	446	623	
14186	44554	A	14269	245	690	APSRSTWGSSTAARRNLKTR KLRTPTPPHKKPRNPHHGPPR TPSG*TPRNPDHPPPG/PQVGG PGCWAPSQGPRGWQLGC*RE EVPGGGHAGRHSTPVGG/DFFL QAGPWPPDASLTPNPFVLRGAS TPPHPLSENNKDKFLQK
14187	44555	A	14270	223	365	

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14188	44556	A	14271	1	687	MSEYIRVTEDENDEPIEIPSEDD GTVLLSTVTAQFPAGCLGR PVSQCMRGVRLVEGILHAPDA GWRNPVYVYVYPKDNKRKMV LGLPWKTTEQDLKEYCSTFGD VLMVRQSQDEPLRSRKVFVGR RTEDMTEDELWEFFSQYGDVM DVFPVKPFRAFAFVPFADDQIA RSLCGEDSMKGISVHISNAEPK RNSNRQ/LRSGRFGGPNPGGFGN QGGFESYQRCERKAV
14189	44557	A	14272	1	833	
14190	44558	A	14273	3	447	RGTAGGQPGNGPALAQSP*WC RLGSGGT*GKSPGTSQGRALPW CSC/SVSTWATAAPGSQQRASP CSWAQPGPLASRLMLPPLR* GHLGHLAWLQLFAAPCPVIHV AVMWSLLGIALRKVHGDWAPL AILSLVVCASNKLNKKKKK
14191	44559	A	14274	988	1803	RAARVPRAPLEAVAHRWASAS EDDGTVLLSTVTAQFPAGCLGR CRNPVSQCMRGVRLVEGILHAP DAGWRNPVYVYVYPKDNKRKMV QSQDEPLRSRKVFVGRRTEDM TEDELWEFFSQYGDVMDVFP KPFRAFAFVPFADDQIARSLCG EDSMKGISVHISNAEPKRN Q/LRSGRFGGPNPGRLQGTRY PAPAPGSPGRAQGLG/AG*SRPS GSWLSGHLQRPEQSVGRAPAA PRHAVRRSLRRLAALCRRTAR CRAQLHVSPQRRRH
14192	44560	A	14275	3	184	
14193	44561	A	14276	1	352	KAAMVRFKHRYLLCELVSDDP RCRLSLDDRVLSSSLVRDIARV IIGTFGAACSIGFAGTIRTCQK FLIQYNRRQLLILQNCTDEGER EAIQKSVTRSCLL*EEEECEEA AKAME
14194	44562	A	14277	1	456	PTRAVEAMVRFMHRYLLCEQ VCDLRCRLSLDDRVLSSSLVRD TIARVHGTFCAIACSIALALARA LNEEGNPEGWRDVAGASAGGR KKGHECPSPCTVFCTLRYPNA YTVIGLLRCKELYQVWWSVL YLMTYLENKGHRYPCCFNTLH
14195	44563	B	14278	34	267	

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14196	44564	A	14279	3	395	SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSLIGILLHL ESELAQTRAEGQRQAQEYEA LNIKVKLEAEIATYRRLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
14197	44565	A	14280	2	1044	SSQMPSPQEGMCGKACTPALS QADSLCPLRLASEVEGYWQM ACAEPYVQSEMNDHLSVWSLQ HGSTTLASMSFTTCSAFTNYWS PGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTSFGLA GMGGIQNEKETMQSLRDLAS YLDVRGLIETENWKLESQIEH LEKNRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV
14198	44566	B	14281	247	857	

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14199	44567	A	14282	1	2104	LRGSELAGGVAAPDPSSRARAP GRGQGSEPPRRS*GRGRAPPRA HTPLDDFPGGRAALSPGRGLSS RRPDPGSAGRPLLLCLRPLHSP PPPRGCQAPAFQSLPSFHLALRL RSSGEEKLWGPRRAAP*SQR RKPDPARPLGAAAAPLRPV*AS D*GAAQVPPPSPLRDGGQPGGR EGVGRRTPHRAAAWLLGE*AA DAAAFHWDGGRPPAAPARLLP GAPHHREDRVHHQPRGHPLQH QSPGDPPTPAGEQHASRH*LCRN PETQKLRH*TSERRDGHREEEH TG TAGVPRSRPATQRPHAVPAG GLQPHRMPLALSSGAASGGEA EHGQLSGRGREEDGPVWPQLP AGLQGHFRGESPRWPPCLGDGS EN*PGPVQAEFSGG*DPVSESE DNQPRSRQFLRLQREEKAKP/D QRFTYLPANVPPIKTEPTDDYEP APTCG/RGEPGVKSSPKTILQPA ARDATRPQLLPRGLPALSAEK HPDASSPWREPQAPRPFSCRHL QGRQCQGPLSPRTAAGRGRPR RPGVPRPVATHPGSPGQPPAL LPQQ*MK*YEMTSPARAPTFC HIGALSSAGVC*LQQTKE*IN *THTWYHSEPTD*MPGAEH*Y VQRLALQEGKQGRET TVSP GGEVIS*QKGGGAEHGRPTV QGP/SHGNPHAV*PHAQPFWH PWGSILEVPYLTRPSGHRIEH
14200	44568	B	14283	41	4224	
14201	44569	B	14284	1	1332	
14202	44570	B	14285	140	215	
14203	44571	A	14286	234	657	VQQPGRGLDLSTDGPGGRSQV GLIWSCCCLH*AASGEPGGRCP GS/GAPGPAGSALEFRARDGVP/ GVGGPSWESHSPAAATPPPAEC RGPPTPSPAPGEAAPEDREDG AAAPGRAEPASIVAPADGSQGG VLATQAGALGA

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14204	44572	A	14287	134	789	PDSSQAPSRNSTRPAASTRKSSS PPAARSAGNELGSSRGDADPPP QNPTGPAPQSAEVPKCD/SSSA WASNGSSISPSFFSLRPWPSS/T KVPGAGHHTPPEGAGGASAR/S SSLAPSAGAPVPS/A*RSQLGTW LSVLRPRL*QSRVRSPPSHVSS PGSMQAPNPSFQPGMNGAWI WWL*THIPLARWPGPPGILVITC PTVTWIKWSFICSFHPT
14205	44573	A	14288	465	1541	GPPKRKLLISNFSKVSQYKINQV KS*AFLYSKK/QTESQIMSELPF TIASKRIKYLGIQLTRDMKDLF KENYKPLLNEIKEDTNIWKNIP CSWIGRINIVKIALPKVIYRFNA IPIKLPMTSFTELEKTTLKFIWN QKRAHIAKSILSQKNKAGGITLP DLNLYYKATVTKTAWYWYQN RDIDQWNRTEPSEIIPHIYNHLIF DKPDKNKQWGNDSLFWKWCW ENWLSICRRLKDPFLTPYKKN SRWIKDLNVRPKTIKLEENLG NTIEDIGMGKDFMTKTPKAMK TKAKIEKWDLIKKSFTAKET TIRSPGSEQKSHTLVRA RL VSD HSQSFEAWLQFLGDTFRGTQKL RDS
14206	44574	A	14289	1921	3199	GYLAAGQVTSRIHTGRRHFSGP ARCPVSCCRRPGC*PQPAVRP SG*HCRKTA PSHGPSIWQTR**P GSWPNLRPG*GWRWLRAPRG RGIPVGC RSNLQLHPTKNPGSH *GSGSPWQCPGVLL*ASGRQPG SPSGGCT*SSGKAGLEPQWHPA IPGKCRNKPAAPASWERAPRPR AHALACGWWRYS SC*SWRS*S SPETPGPAQV*CHRPCAAW/W RCHS**TAQFL*D*FS*FLQTIGE PCICPKPISVPH*PMKQSHRGIG GCLQYSSHPGIESLGM SRGF/D RRDL*TLQIGS*RHPRAGPEGA AL*CLAGESSLRTPSAPCPGSPH TPGSSASGNTSPV**ETGCGSRQ GSARLVLESLLSR**CLSGPSRP SCLLRGISWQCGTAGRLSSSGPP AASGAGADAAPGGFPRLPCLEF GTV
14207	44575	A	14290	3	626	

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14208	44576	A	14291	1	1065	MRGSCERSGEDDEEQKEEAMVA CGRLSGVPEAEQGP EANWDS LETEGTDGLGELVRD TLYLRSC RAHSVVPISCF LRQGS AQELNL RHRGLGPQGARALASSLSSNPY VKRLDLRDNGLCGAGAEALAG AL/QQKQHP*CGPVGEPAGSG RSPGP/RVPPSQ/CNQAMRKM LSGNGLEEQAQHLAE LLAH TDLKSLDLSYNQLNDQAGPAPS LRAFPQANIFLKVLDISYNGFG DPGASAVGEALKANNVLEELN MSNNRISAMGALSGLGLRVN QTLRLVLCVRVSQVSRNPMRS EGCFGLLKSVDNPPASALELDD FSDIQVNAEFDGLASSVRGILPG LGIKDWRLQSGV
14209	44577	A	14292	1	416	
14210	44578	A	14293	2	384	ELWVVTFSFMAYGSAKDLICTH FMDGMNELAIAYILQGV LKAL DYIHIMGYVHR/DLQGYDAKS DIYSVGITACELANGHVFPKDM PATQM LLEK LNGTVPCLLDTST IPA EELTMSPSRSVANSGLMTA
14211	44579	C	14294	142	474	
14212	44580	A	14295	1	1470	
14213	44581	C	14296	91	471	
14214	44582	C	14297	195	480	
14215	44583	A	14298	121	1130	SRSTQYELMSFLTNDASSESIAS FSKQEVMS SFLPEGGWYELLTV IGKGFEDLMTVNLARYKPTGE YVTVRRINLEACSNEMVTF LQG ELHVYKLFNHPNIVPYRATFIA DNELWVVTFSFMAYGSAKDLIC THFMDGMNELAIAYILQGV LK ALDYIHIMGYVHRSVKASHILI SVDGKVYLSGLRSNLSMISHGQ RQRVVHDFPKYSVKVLPWLSP EVLQQNLQGYDAKSDIYSVGIT ACELANGHVFPKDMPATQPM VLVLSPPDAARETERHSALPVG YQHHPR*GADHEPFALSGQLW PE*QPDHQHPALQR*LALPPLP PNLLPPLPPLC
14216	44584	A	14299	304	412	
14217	44585	A	14300	2	350	
14218	44586	A	14301	191	299	HRPATAVLHVPTSPSPSGSRPS *PPPAALLWTPA

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14219	44587	A	14302	537	5523	LARYYKFMHQDRQGVARNLL CQKEKRR*YTTKCEDNTCHWT GRTSS*PRSV/SNLNSQCQPRLW PPVTIIRQANIKTGEKAH*TSKL LPPVQLKFPARDDTLPPWPGYIP* QLRRPSPR*SILSMLPRKVVPCL *QKP*TVCWKF*EPLSYIIHSLV LKMMIPMPMTLLGA*CLTQAL K*SRMERKKGRAAQRSSLTGC QSPRGSPGGPGPPGPPGAGKQ QNSNVQTSRLLARTLI*SFSSST VKDKELARNTAP
14220	44588	A	14303	2868	3095	PWAGGLFGPSAGMRAWATK PSLTPPAPAGQRCPCQGHRG*SG PGIYAVQPPSVPAWAAHATTQ ARLCHPRSPPLR
14221	44589	A	14304	693	821	SDRQT*RQEKRLTRRQSCCLPC N*SFQPETTLFHGPDTFHDN
14222	44590	A	14305	338	645	
14223	44591	B	14306	181	480	
14224	44592	A	14307	155	543	
14225	44593	B	14308	1	1260	

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14226	44594	A	14309	1	2025	VINIINAAQESSMPMPVTEALDRV LEILRTTELYSPQFGAKDDDPH ANDLVGGLMSDTGLEIHKDGEE EGESRTAQQYPGLSESTRQPWR RSRTPTTTGWGKATEQCCPDF PPPGPHPLELLIFHCEGQGTGQ KHSTSYPTLMSEKRGMLNVPF AKYTGPMARKSSGLTPSLHLHY CADPLHSKPLFNCPPTTSKTEI LGSNCNCPSESVRGAEGDQEL LANIKQAEKHEKNHPEVTVM ALTDIDLQLQFSMSQPEALLL AAGPADHLLQLYSGHLQSAT GIYGEGRASSATLEDLESQYQE LAVALDSSSTIISQLTENINSLVH TLKEEKHEIHQVQKLGRNLFKL KNQTAEPLAEPPEARPSKVEQL QDETNLHRKELESVGRQLQAE VENNQMLSLNRRQEERLQEQ EGWQEEQERLLDKNNENKSAL QLEQQVKELKL\ENLEATSQ*K QQL/TAQLSLMALPGEGDGGG HLDSEQAAPRPMNPNGDLESR EAMVAFFNSAGANAQEEQRVC CQPLAHPVASSQKKPEVAAPAP ETGGESVCGETHQALQGAMEK LQESTSARGQCQRSTGRGGHR QAGPGPGDEEMLCCTQVSS AGRGMGMLTVVLVSLMMLS ASFSTWCMRSISSCHCAYSAS SISVFWFPREYILASGSEMMNS
14227	44595	A	14310	3	564	SLRVSLKAVVDRAGRSILSYIA GLGVDLFGGGGSRVAGGIADL GRSGGKATRSRRGSRAGGGR LRSRIHEEALQLRETPGGAPE\ PMDQYAGPGYDIRDWELRKI HRAAIKGDAAQ/VWSAAMTRR FRDLDAARDKDRTVLHLTCAH GRVEVVTLLSRRQ\DICD/N* NRTPLMKAVHCQEEA
14228	44596	A	14311	515	778	GQAQGTGDREGAVLFTARAPD QCRP*SCSSSRPTASSCPLGHSC SPGPLCTHLPLQGPPQAPTVP ATATCWFSWNQCRCAVSSYP
14229	44597	A	14312	411	608	EAEI**TGLPGHSRPPGPLCTHL PLQGPLGAAAWVPEAGLGQVP TEAAGARAGCSAHKPWKRRK
14230	44598	A	14313	2	338	
14231	44599	A	14314	1	390	

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14232	44600	A	14315	237	488	PWKTLDSSEAEILRGVSESSAV TLHCMEGQAVGPRQVKRIVHC *ASSA*NPHAMLLQNR*LALC TSVPQGA AVL CGGWDPGN
14233	44601	A	14316	358	616	
14234	44602	A	14317	13	1155	IKLPPPGCRRRGRHRRHRYRG RAEPLAPRRRLPPAPEQPRARP PASRFLKNTMSNGYEDHMAED CRGDI GRTNLIVNYLPQNM TQD ELRSLFSSIGEVESAKLIRDKVP GHS LGYGFVNYVTAKDAERA I NTLNGRLRLQSKTIKVSYPSS EVIKDANLYISGLPRTMTQKDV EDMFISRFGRINSRVLVDQTTG LSRGVAFIRFDKRSEAEAEITSF NGHKPPGSSEPI TVKFAANPNQ NKNVALLSQLYHSPARFGGP VHHQAQRFRFSPMGVDHMSGL SGVNVPGNASSGWCIFIYNLQ DADEGILWQMFGPFGAVTNVK VIRDFNTNKCKGFGFVTMTNY EEAAMAIASLNGYRLGDKILQV SFKTNKSHK

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14235	44603	A	14318	1	2340	MFVWRNVEGHSAAVFSWYSIP FLTPPCSHTRPSNLVPTQWPTR ENNLPSWQPLLMSVHQAQSL ALRKEQDSSEKDGSRPNKSDK DHIRWPMSGADHLQQAAPGPG GAHQGHPNQDNRTVSQMLSER WYTLGPNEMQKYNLAFQNV ARIRYVIVRGNEQGGFRMHHLR GVSSLQLGRRRPGPGTYRLEV DMITIDARYRCSGLRSPDPDH LKSVDLHRNEHFFLQKARWEIH LVLQATPSQIQLLHVAFVLAQ PLRCRKQTLFLISVVGTKENNV ASEGRNPVRPLRGHRWLPASP AAEHFAGGADRKSRAPRSA ATATPANEQRAVADVQWAR ARGGRVRAAGRSGSCALRRSR CRRRRRRHRRHRYRGAEPLA PRRAASGQPGKLARRGINCNA SSIPMLQVVRIKSISKHCQMAR VAGEGSLPLSHAQLTHCVFGN KQVQRTIAYLPQQQGVQGLF KNTMSNGYEDHMAEDCRDGI RTNLIVNYLPQNMQDELRSFL SSIGEVESAKLIRDKVAVGGLSL CVPIRNVEIVASTSWWSLPLAP YVPRGIRRSQPTLMDLSCRS HQAAPFTASVLLYISGRVKAH TAAQGFNHIPEEGVSQEAAGS WSQAWKDGWLTNVFMFSGTG HSLGYGFVNYVTAKDAERAIN TLNGLR/PPVKNH*GRPLQLGFL
14236	44604	A	14319	701	1050	LIVHFCLQVGGCGVNTVFPILQ TN/NTNSEYDPSRCFAFVHDL DEEKSYVPVKSSLDIILIFVLSAI VPDKMQKAINRLSRLLKPGGM MLLRDYGRYDMAQLRFKKGIL KVLNPNH
14237	44605	A	14320	701	1519	LIVHFCLQVGGCGVNTVFPILQ TNNDPGLFVYCCDFSSTAIELV QTNSEYDPSRCFAFVHDLDEE KSYVPVKGSLLDIILIFVLSAIV DKMQKAINRLSRLLKPGGMVL LRDYGRYDMAQLRFKKGQCLS GNFYVRGDGTRVYLCHTRCNW TRFSPTAGLEKPKPVDRLQ VNRGKTTDNVPGLDSSVILQAP SVQHQLRGYLLPTRCKPVVVS GLFLKKKIVALGVV/RCL*SQPL RRLRRGGSIE/HQQSNLGKIVRD PVSESNDKIKRI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14238	44606	A	14321	756	1334	PGKFVLSFLDPQPPTRILEVGC GVGNTVFPIFTNRTMTQDSL VYCCDFSSTAIELVQTINSEYDPSS VFVAFVQGPV**RESVTQCPRAV LDHILIFVLSAIVPDKMQKAINR LSRLLPKPGMMLLRDYGRYD MAQLRFKKEELDITFTAGLEK VQNLVDRRIQVNRGKQLTMY RVWIQCKYCKPLLSSTS
14239	44607	A	14322	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
14240	44608	A	14323	1	5796	
14241	44609	A	14324	1	2721	
14242	44610	A	14325	1	3438	
14243	44611	A	14326	1	3306	
14244	44612	A	14327	1	2364	
14245	44613	A	14328	1	2091	
14246	44614	A	14329	1	2334	
14247	44615	A	14330	1	1986	
14248	44616	B	14331	1	2559	
14249	44617	A	14332	1	1671	
14250	44618	A	14333	1	1845	
14251	44619	B	14334	1	2055	
14252	44620	B	14335	1	1554	
14253	44621	A	14336	1	2559	
14254	44622	A	14337	1	1714	
14255	44623	A	14338	1537	2204	

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14256	44624	A	14339	2004	3751	YQSLAETQQQKKNFRPISLMN IDAKILNKILANRIQHHQKLIH HDQEGFIPGMQGWFNHKSINV IQHINRTKDKNHMISVDAEKA FDKVQQHFMLKTLNKLIDIDL EVLARAIRQEKEIKGIQSGKEEV KLSLFADDMIAYLENPIVSAQN LLKLISNFKVSGYKINVQKS/Q AFLYTNNRQTESQIMSELPFTI ASKRIKYLGHKLRGVKDLFRE NYKLPLIKEIREDTNKWKNIPC SWIGRMNIMKMAILPKVNYRF NAPIKLPMTFFIGLGKILLSSY GTTKRAHIAKTILRQKNKAGGI TLPDFKLYYKATVAKTAWYW YQNRDIDQWNRTEPSEIMPHIY NYLIFDKPEKNKQWGKDSLFN KWCWENWLAICRKLKLDPFLT PYRKJNSRWIKDLNVRPKTIKTL EENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLSFCT AKETTIRVNRQPTKWNENFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWVKDMNRHFSKEDIYA AKKYMKKCSSLAIREMQIKTT MRYHLTPVRMAIKKSGNNRC WRGCGEIGTL
14257	44625	A	14340	519	1286	LNLEERAFRHKSSEHLPHLKVH FRHSSCGIKTSLHVSPTTLIF PYPPLWGNPSN*ARPPCSVHSG PYPQGLASIIAHGSPGNVRGVH V*INDEGGISRPSTASHKETPR PPTPARHADLAATRPSLTTPSPS VGAGPRA/PSRAGPSVGGGLGRP SGRAPRAEVALPAGLSPAGLAG PPPSGRSTGALPPAAAPTTSGP/P ASTPPNAPAGHTLSSRSPhRA ARPPHCGAEETWGFTMRPSW RISQSFTVKDS
14258	44626	A	14341	482	700	

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14259	44627	A	14342	1368	2416	SSMTQSSCPMTSYLKSKEGPEL MPSYTNPTETGVSKLVNKTQVF TYAHKGVPVSIFYDACQAAHLSK LNNIWTISVKI*DKKESASRATK AITEESKKECPDCDNQWTTHEF NQHLTYGRAALFASQEEKIGYT TGTCYPLNLTLKPNMTFWTKG HKGLLTFDQAGALLGLPLVI TKKTQRTQVQLSPIQQFRFYKS FNEHFNSEVSKIQIPPISTENLFV QLAKSIANNLGVTSYVCGGA NMRDQWPWEARELMLQDNFT LPEFVTKFNANPSVWLLRNPIIG KYCIACWGKSFQNIGETTCLG QQYFESENRTQWRSFIDDSIG HFNPLQFPTLNQSWYQLE
14260	44628	B	14343	1	1071	
14261	44629	C	14344	89	283	
14262	44630	A	14345	244	315	NPKGQKQDREAPLSRSVFVLKIKI KRAFALLHGRF*PSTPAASASP ASKSPRGSGKALASALFYIVQL TK
14263	44631	A	14346	1228	1656	QVYRPSQTPHLALSPERVAPGR RAAGRLAPEARAPRGSP/LPPHR VSEKTIRVVVFHGPARRAGGTP PRAPRGDTGGAPGA\PTYSTPL MSLHRRARLESPTGSSFPADSA KPVPLAVVSLDSR*GWESRSS IHAIVTN*MTRI
14264	44632	A	14347	2	705	GSWFGLDDGSATRILACPWPGL GDGPAAPKANLPLVRWKPCQCF RGEGL*GSSCFSATLLTGLDLW ACCSSRSASARLSTYPSAFTSG WCSSLGPTEEAPGSWINCLAG ILGAATSPKPSAIPQASPEVSLD AEDTGMKP*DSA/GPPGPARGL CGRGGLSPACMGLRP/PSPPA QSPSTALTSLTPSPFHPPRKKW SPPSAPAPSAPSAPASLTSPAP PAPSPAPTAPAP

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14265	44633	A	14348	367	1174	WVRGQPSQSLDLLACSTPTS* WPPGRAPPPLP/PPPPLP/PTP ASPLLHPRRAPPPVP/SFTP ASPPDPVPRPTKALTGLP/LCP LPCMGR/PFVPYLGGLPCLGP DFSSL**SPGGWDRPVRPLGISQ IPE/PPLTMGL*MQ*IPP*PRFQG HYAPLPPLQTLICISVKTGRNPR GLPMHKILQPQNPSQPPCELQ AHCPTTPPPKQCP/PAAFSILPVT FADKDPGAAPEGTVKAPMPTQ *EL*PLRPREHRVLSGPTAGQT
14266	44634	A	14349	332	988	RRAGTPASWGHNGARAKTPSR ACACGLYPIHQPTARRAPAAR SHGPGPPALPRKGAAGHGRSVS HHPLRPCSRSSCLAWPCLHHQ PLHCHPHRHWPKWHPHLAPH PLLGLHPRSRPQTPPWTS CGPSR RLPTPGSWPAPFDRDWP*AR PSALCCPFCQEPQLTPCLHLCPH PHPHRHLPGLSCPHRPPRWRSP QSPCPWVLLWWTGQWWQPG
14267	44635	A	14350	190	718	FVLQLPPAPKSGLGRWGSPPPG QFSSSQRTGTVRGRGCAEPRG SLPHPT*GNNK*HGNWMGLGS QGLGRQPGEDKH CYQR/IGV GAHLLRPPHQIRSLSTGSGCS HPWSRELGCSDQGRASAPLA LRQAWGEGLAGRNHTIVPFHG DISIAPRLLPCRETLSALCGGES
14268	44636	A	14351	1	486	MKGEVSCQHQDALQQVLWA MLQDADKQVRAPGPVENENH CDFVKLRMLICTNMEDLREQI HTRHYELRYRCKLEEMGF TDV GPENKPVRLVLLFKSLSDSKRVK YDEEWIRLPVE/MKY/MLERKV TQKQP*VPLVFVSWRSR*ESLR REEENQQCHVLEL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
14269	44637	A	14352	1	2380	MMWSVLIQPVVLA AVERQGE ALEFLIGVPESDGENGTKLENT LQDIIQEDFPNLARQAHVQIQEI QRTPQRYSLRRATPRHIVRFTK VEMKEKMLRAAREKGRVTLK GKPIRLTADLSAETLQARRDRG PIFNILKEKNFQPRISYPALKSFT SEGEIKYFTDKQMLRDFVTTTRP ALKELLKEALNMERNNRNFFG VTF AFFVGGQSLGKALQETSIPP LREEDLEKTSILETNGDWEAT RGLPEECAGMRERDCQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAAGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNA GRVFKDSD KFDANDPILKDQTEWGSATF TSDGKIRLPYTDYSGKHGKQS LTTAQVNVSKDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGGH KYLGLIPTYDISSNIYLSKSLCW QANFRLNSALAQSPAITNFQFR GHSLKTLDLLTMKNLDSKVNI PVIKADTVSKTELHKFKIKFM SELVSNQVQIYQFPTDDDTIAK VNAAMNGQLPFAVVGSMDEIK VGKNMVKARQYPWGVVQVEN ENHCDFFVKLREMFICTNMEDL REQTHTRHYEL YR:RLQLEEMG FTD VAPKNKPASVQETYEAKR HEFHGERQRKEEEMKQMFVQR
14270	44638	A	14353	105	328	
14271	44639	A	14354	107	676	IRPDSLPSASPAQDFYAASNTF PA/DRWSALT KIYEDQTSNINPL SQ/TLIQSKALTLFNSVKA EKDE EAAEEKFEVTRVVHIRGLIDGV VEADIVEALQEFGLISYVMVMS KKRQALVEFEDVLEACNAVNY TADNQIHIAIGHPAFVNYSTSQKI SRPGNSDDPEREQCASLYHPEP HLFDHHGCSLHYR
14272	44640	A	14355	221	648	LDWLRRVVGIPSLRWTCATLV GTRRAARHRCVNVWECGGKKE ITY*SV EGLCRA/EKPKPLALLE ETCKLPERQVVNAKEKFL EELIK SATPVNT*MIRKRNCIITDMEK V*AVWIEDQTSNHLPLSQSLIES RALTLFNYVMA
14273	44641	A	14356	122	317	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
14274	44642	A	14357	338	489	WLGQN*RHGKQPGPGVGHVGT TVWS*PHSPACWAPAPQGPAPT GEEGCHF
14275	44643	A	14358	1	459	RPVWRNSQPPTAAAYRWASGSR MWSTSFSRW/NKTPSGKACSSS DKGPPMAQVPIQQRNVPPPTK/ QPLVLCHGEAPDFSRPPQHRPS LQKHPSGG/PSHSPLPTSA PSSR AGLPLAMTLDLTSGWRLWTPI QPFRLPPGSCREGTILLCSVMD
14276	44644	A	14359	609	2077	GLKAQPSRRGHSRGPACAAA PASRVHLPVTFCEPNSSPCPHC TGGWGGRGQ/PACAGNPTASSP CQIECPALRSCLHALMDLGSQA LRGAPRTGVDPRLHLLPQPAL SSPPVLLRGPLLRTCLAAARQ GQSPAPGLLGHPGSHRGLPP AQGGHRLPQPPGPGRRHRAPQP DPRRPGLRAAASGPGLAAWG AVRAAERPGSGGLPGGAGPHH ARAQPGPRAAPAAAAPGVAP AGGGA VPGGHPHRPGGEAALP AHGLPAPAAERTAPR/QPCPAC GLIARSDVHHPPVLP/LSGPAP APGRLVGQLGVRGAPSSPVPH ALHFPRAQ/PPGKGITTTSTQ PAGSPSPCMPPAATPG/ARHPP GSA\GHRAGV*GHTGPCDPHGP GHIHGAQLL*/DQAAVGVGRP GPWALSGMSQPPT/LPTAGHPA PACGVRAFDGTRPPRAKPAL/ LSDKGPPMAQVPIQQRNVPPPT KHPCPGPQSSTWMRQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14277	44645	A	14363	47	1250	EPRPSRSSGGPQLGQGLPRPMK KIPGSSAKTAGPLATRPEVPRAP *SAGRQPFWRPWPWGKRKGRKT *NHGSPGVK/TPGPLNKDKGE KEERPRQDQQRKALLHMFSG KPPEKPLPNGKGSTESSDYLR SVTPGPWSFSPQVASGPMPPVH TTKKPA*APPQVL/EPKERQTGA AADMPQPAVRHQGREPLL VVK PTHSRPEGGCREVPQAA/SQNPR PAPGLQTPGTRQTS/SVTPQPCP PAATHSLGLGNSLSFGPGAKRP AQAPIQACLNFPKKPRLGPFQIP ESAIQGELGAPENLQPPPAAT ELGPSTSPQMGRRTPAQVPSVD RQPPHSRCLPTAQACTMSHHS AAGHDG/DPASQSALPETGKRT LELQPPGGPLISL*EAGLSRSE PSCVREV
14278	44646	A	14364	23	714	EAPEIPRQNRMTMKERPVL PHK*IHPNVAKWSRVPVQVQK NPQFQEPTPEFIPVPGTSPEAAG FWH*GAHDSPGTRDRSEVEPGR GHPHLGPRDSAAADPGEHSPCD CP*ACPEVRRWPAAPVQIQYIIP SVDDFSLEFHAQDGDIDMRRE NVPFSPAEEGKAAPLYQQPLMI PQANHMAGISPS/PTAAEFQHR DVHHRGPGTRDRTHTETGRVC PHPVPTDSPAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,117	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14279	44647	A	14365	3	1869	ITTVAPSRPASSDCESDGS*EQD AGPGSRMGPEK*AGPRPTRRVG RWSQTHSQDDTSGAVVPEYP SDR*YAGGRGPG/PGGPTVHP* KRRS*NPQETKMMARRDPKSW AKRLSPV*PRLAALLTSASPSCP LEPRVLPFRVPPSHGLCEGTSYP NSPGT*RPPCRSSAKTAGPLATR PEVPGAP*SAGRPWFQRPWG KRRG/GKPEPMEAPG*SQPGAL EQG*GREGRETKATRPAAEEGSP PHVFRETREAAAEWKRIHGVF *SSEGHGP*FPFSFPSAGGNRGT PLSCLLGVDRDSTILPGCKRANA GPHNQ*EAARGPCPR*SIAAE MSGRGSVLASLPLRKASLSSSS SLGPKERQTGAAA/AHPSACSQ APGPRASPRGEADTQPPRG*LP RSSPGCLQNPRAPGRQTPGTR QTS CGDL/SSPARQPHTAWA* APISASGQEPRDLPSSDSGLPEL PQETETGSLDPKRKHPRG*AG GPGKSPTSASRNRTWTKYVAP DGQEDTGPGAQRRPAASAQQT LPA YCPGLHHVPSLSGQP*WGP ASQS/GSSGDWKTADAGAPASW RPPHFTLLRSREPSLRLMCQR LRLLPVFVSHRASSMRTRFPPPP QRTAILTWS
14280	44648	B	14366	1	1519	
14281	44649	A	14367	312	1326	TTKTGQDKDRLEEFMSQQLSGS KRMSTQPRTELPPNRHTTTTS TTPA TNTTCTATVPPOQYSYH DINVYSLAGLAPHITLNPTAHP QLKQCVRQAIERAVQELVHPV VDRSIKIAMTTCEQIVRKDFAL DSEESRMRIA AHMMRNLTAG MAMITCREP LMSISTNLKNSF ASALR/PDGSSAIQL*SNDS*SCS WRPKLYDAFWDLSLRV**PSR PEGEGRVSEGMGESLPFSSSW PRQYQSFLCICWTDAPARNTED R*SHNKVLSSVY*NVC*NQLPC SG*AAQSCCQSHHDPQVLSQ PGCLCSTHCTARETLRGGHQHC HKD*SAEQGL

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14282	44650	A	14368	2	1120	PEPEPGARGGEQLNEDFEG*VA VPTCLHCPALSRQTQRAIQALT VRRGEATIRPPPCDDTKGGHFR LNELIKVVSPKVGAPSPSSDLPC RMWGEERGWTVGLPEEVKIAE AYQMLKKQGEAHRGWGATRA CLPLPHHERPKNVIFEDEEKSK VRLQGGTYGDSEPRWGSVGS! KEMVQF/DSGRAQSTGRRRDG GIELGHNVKLLTEMVMSSHSG GAAAGSSEDLMKVHLPCLPHS LPTPQPTRTLRMRPTLFLASDT EDNDEALGEPRAGAEVRSPLP PPPAPVRGEEVNGDATAGSIPI EEVAGELGGHPSGWRGTESYP AMPTRPGEQASPEQPSASVSL DDELSLGEGARPGGGRAQQ
14283	44651	A	14369	1	432	GTRQEVTAGVEPAREWQRRLM EVQWGLERAPYCIQHAPR*RRS PARPGTQSCGLGACWIO*GALS SPHCTSISRCHSLAGSTPAVTS CLV
14284	44652	A	14370	16	471	
14285	44653	B	14371	66	206	
14286	44654	B	14372	234	390	
14287	44655	B	14373	207	427	
14288	44656	A	14374	2	572	FLLERAPYGVGFSLLPGLWLGS RAGVGRHHDKRVGLGRAPTWS LEGAVSSM/TPRPQLCVP/WPC WGPSSPGG*QQLGQLSCSYSLV DR*VALLWFWMLVGSPLVKGH CPTPWSRFVDFSVPLATPPGIVY WGLFAVFLFSHLLPARPGEQMS ACCRHLHAPSSPLLTLDSLKVY SCNSQGLVVRVFPFGD
14289	44657	A	14375	175	499	KQNKSMGRKSQGFVASFNGHL YCTASCGMPASSTSTQTWPRVL PLHSQ/ESSHGCSWRGRR*GP RPRPHKTPVPMVMDSTARNRA RRELVLAWCKSPLATALLVSW DK
14290	44658	A	14376	408	625	VFGQEVEFGYMNKFSSGDF*DF GAPITLSSEHCTQCVCVFPYPSAP SFPFPVPKVVHCVIPHSLVPTYE WEHTM

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14291	44659	A	14377	1263	1812	AGDAAPEDPAGRGQEDLYDEE LPGWGLCIPHACLPQCHA*VT KAG/ARVKVILPS*DTQRTKDIL KAGGG/PSSIHFINSAHGKPAVI VRPRGIWVLNITPLSGQWGPVI GVYTAATVDMKSLGSGSLGLQ LALPLAASWLGVLTEAARVFG EQVVFGYMNSFFSGDFWDFGA PITRAVYTVPNV
14292	44660	A	14378	1	693	WDYV/KRPNLRLIGVTSDEGEN GTKLENTLQDILENFPNLRQA NIQIQEIQRTPQRYSSRRATPRIH IVTFAKVEMNEKMLRAAREKG RVTHKGKPIRLADLSAETLQA RREWGPINILKEKNFQPRISYP AKLSFISEGEIKSFDTKQMLRDF VTTRPALKELLKEALNMERKN RQINETENQGGYPGIELGSAPEG PNPLFCRHLQMSVDGRHLQNSP PQINRIYIFLAPHHTYSKIDHILG SKTLKKCKCRTEITNYLSDHSA IKLELRIKKLTQNCSTTWKLNH LLNDYVWVHNEMKAEMKMFF ETNENKDDTTYQNLWDTFKAVY RGKFLALNAHKRKQERSKMDT LTSQLKELEKQEQTSHKASRRQ EITKIKEELKEIETQKTLQINES KSWFFERINKIDRPLARLTKKK REKNQIDAIGN
14293	44661	A	14379	2	1299	
14294	44662	A	14380	2	383	
14295	44663	A	14381	1	1536	
14296	44664	A	14382	2	1118	REHLAEGMAVGTSADLNISA CWLRRQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFORK EQAAIFA VLPPLVIPRKTTGSGV DLEQTPADLQKRGTLVTRKTN KQKAIAISTSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSPAR EQNWTENEFDELTEVGFRRWV ITNSSKLKEHVLQCKETKKLD KRLEELLTIITSLEKNINDLMEL KNTAGELRDAYTSINS*IDQAE RISEIGDQLNEIKCEDKMREKAR MKRNEQSLQEIWDYVKRPNLR LIGVPESDGENGTLENTLQDII QENFPNLRQANIQIQEIQRTPQ RYSSRRATPRIHIVRFTKV

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14297	44665	A	14383	1	1154	MLPILGSRHPSSLGQARKLDYR PSKSQCLEPGTPRACLVITYLV AKLIYNDYFIHYFAPRGLPPME KNVVFVIDISGFMTGKMKQD HNFLSAREQNWITENFDKLME VDFRRVITNSELKEHVLTOC KEANNLEKRLDELLTRITSVEK NINDLMELKNTAGELREAYTSF NSCNDQAEKISEIEDQLNEIKP NLRIGVPESDGENGTKLENTL QDIQENFNSLAKQANVQIQEI QRTQRYSSRRATPRTHIIVRF TKVGNGREKMFKGQPGGKGR VTLKGKPIITLADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKYFTDKQMLRDF VTRPALQELLKEALNMERNN RYQPLQNHAKM
14298	44666	B	14384	1	1554	
14299	44667	A	14385	1	909	
14300	44668	A	14386	2	207	DIMSCILQNYNRPVMAIAPIA VKFLHRGNKELCRNMSNYLSL AAITKADLLADHTEVIVKSILQ
14301	44669	A	14387	496	1207	PLITGTHDSGSVESQLIKLILTM HQLFRLVLGQKDLRAGDLFS *NNEIEDSLTEALEQIKIHSSSD YQTNNNDQAVVEICITRITAIR ETESIEKHAKALVGLWDSCLEH NLRPFKDEDTPHAKIASDIMS CILPELQPTFQSMALAIPIAVKF LHRGNKELCRNMSNYLSLAIT KADLLADHTEVIVKSILQGMVR KLSLGTCTFGRYLKVFSSSIYGL WEARPRVLEAN
14302	44670	A	14388	219	448	VSLELCLKTTGPDCCGQTSQTP PAAAYHHLPAGAGLPCGRLPA LCCSCPMGARPL*HHKR/DPSRF QEKTHLYLPSSH
14303	44671	A	14389	542	1365	GTEGVMANRSQEGNGGGSWR AKQVVVTVPF*EQSLVIMLWR RGNT*QRPSEGTSSSHCSFH MSRHQ*CKCLLKPE/VSAEAR DALDTKTHFLAMIPSYLLNG NIGELPEGPAGGCAQNPGLWAS /RGPARR*RSQASSPEVRWPPG QCGLRGRPKCKE/PRPHWPSP CASPYRGAGGQRLRACSAAG RKTPDRRLPEPTRGPVSQRAV LGKLRAAAGHRIPIDGLDGLS LGAPPAGRHLHTVPLRREFSP CEDALGIGEQQKKRV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14304	44672	A	14390	3	723	PVLRGGIQEFAYIKALYERKFL VPKPIDYNRHAVDMELINGVPL C*IIHHVEDPASVYDEAMELIVE LANHGLIHGDFNEFNLIILDESD HITMIDFPQMDSHTSPNAEWYF DRDVKCIIDFFMKRFSYSESELFP TFKDIRREDTLDVEVSASGYTK EMQADDELLHPLGPDCKNIETK EGSEFSFSDGEVAEKADEVYGE NESERNCLEESEGECYSDHLETL NK*RKTVYQKRVLMHGVLLK
14305	44673	A	14391	I	1889	MGSKVKEVEDDSQMSDLVRG MNAFSKTGSGGVEQGRGTGQGG TNGHIKKAKARDRRRFFKTP QRKVGNDNLQLPLRWTEQHAE THIMNFCSKNYNRNIPGKPRESI DTLNEAACRGRLSKTARKLWS EAQDQRSFQATEMQAFLFSAK RIAAEKKTIIRRRDLCSIWGKLL PRPGSQSVPAQIPENLQEQEERA KWLNLGRSKFFPQTSTLKGVT SNKTGVKEPELESRQPNLLKVE MGMKNHIEIVPGSLIASIASLKH GGCNKVLRELVKHKLIAWERT KTVQGYRLTNAGYDYLALKTL SSRQVVESVGNQMGVGKIESYI YIVANEEGQFQALKLHRLGRTS FRNLKNKRDYHKHRHNVSWL YLSRLSAMKEFAYMKFRTLEIR DYFYVWKINVLTPGCSPKRGSS GEFVPCLLQLLLGFGDCWHSFG LWHITPVSVSMLTLLPSLLLVK QKKPTLDSRMGQDFVVELQL YLCVLEREVIREYPPDGQIFGRY FDRDVKCIKDFFMKRFSESEL FPITFKDIRREDTLDVEVSASGY TKEMQADDELLHPLGPDCKNIE TKEGSEFSFSDGEVPEKADEVYGE SENESEERNCLEESEGECYSDHLE TLNK*RKTVYQKRVLMHGVLLK

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14306	44674	A	14392	150	1910	STPPGGPSVLM*STEEPGAGRS QPLCDDLSTRPLSCLGAGCCLW PAKRISAKEEPWYSSRSKDKKE KNYSSPETTTSGGCHSPGDSQY QELAVALESSVTINQLNENIES LKQKKQVEHQLEEAAKTNNE IHKAQMEQLETINILTLKADL KTTLYHTKRAARHFEEESKDLA GRLQYSLQRIQELERALCAVST QQQEEDRGHCLSSPDQNFSLFTI QSSSCREAVLHRLQQTIKERA LLNAHVTVIESLKQVQLERD EYAKHIKGERARWQERMWKM SVEARTLKKEKKRDHRIQELER SLSELKNQMAEPPSLAPPAVTS VVEQLQDEAKHLRQEVEGLEG KLQSQVENNQALSLSKEQKQ RLQEQEEMLRQEQAQRVREQE RLCEQNERLREQQKMLQEQGE RLRKQEQRLRKQERLRKEER LTKAGKEAVGPGGEAVEEGGE ATKAGGEARALPEPQARQAAG RATVQLRGSEQREKERTAVGA ASKGAAGEARRGEGDAVHGHL SAADL*EGGAAQAVTAADPVR GPAAAAGSLGQSGAPRSCQPPE PTARDPAKPRGSPWRRRWRTT
14307	44675	B	14393	463	3755	
14308	44676	B	14394	175	1835	
14309	44677	A	14395	102	465	RAYCWAYIRLSCLTVILIAWCS QESALSEEEEDTTRPLETVTFKD VAVDLTQEEWEQMKPAQRNL YRDVMLENYSNLVTVCQVTK PDVSSWSKKRSPG*WRKKCL GGTVQNPEERTAV
14310	44678	A	14396	1	330	
14311	44679	A	14397	1	531	MLLNIPQIHTRQSPRAKNYLAQ NVNSVKAWCQESALSEEEED TTRPLVRLKHLFVSCILQCSYV LLPLTPEYQLNKFLYVVTMPN FDDFKLISIMFLQETVTFKDVA VDLTQEEWEQMKPAQRNLVR DVMLENYSNLVTVCQVTKPD VSSWSKKRSPG*WRKKCLGG

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14312	44680	A	14398	1	539	MPTTTTREM TQNSSETIKNKNG KKQRKQRKNSKKNRKQKDE DKTRRQNKRRHKKNDINPEEE RTAVRLKDGGAAPQAVQEHD AGICASGGAQETYILVEGKGE ASTSPGQSKGSGREGGVGANETC SKKLYRDVMLENYSNLVT/VG CQVTKPDVYSSWSKKRSPG*W RKKFWEALSR
14313	44681	A	14399	322	1227	FDLKMSKCRKTPQLQASPAF SPDILADIFELFAKNFSYWKPL NNEWQLPDPEIFTCDHTEFNA FPWI*RTP*NEVKKPTGVIRTW DEWHEHTCFH**SGE/ISFPHGR KSVNAELWTQAWCKFHEILCS FPLIPQEAQNGKLNLSHLCEAP GAFIASLNHYLKSHRFPCHWSW VANTLNPYHEANDDLMMIMD DRLIANTLHWYFPGDNTGDI MTLKLFTGLQNFISSMGTVHLV TANGSFDCQ*NPAGDQRMVKG HCYFSPWNWLHLSKHTQCGNE FIFMTKKKQSLTAKSLPDTFS
14314	44682	A	14400	3	183	KRKEITNSLDAASRGTVPAAL AGVQYLEPRAGAAGRLGGAG WGRVPRPGSS/SSLVLGR*GW CPV/LRTQGRCCRPPGGCWVGA RPAWELLSLVLGR
14315	44683	A	14401	21	399	IWNSAPTASRRPWSLAPGSPRS TWCVASTPPCAPGKAREPRDRS EVPPATAPAVLQSHWPCPRSSR SGSAGNCVGPSPHWSAPGHSQH LTPGPGHGGPRGP/CWHLLMQT AWPALTPPGAMPGEAEGQ
14316	44684	A	14402	59	478	RCSQPWHCPAALAGVQYLEPR AGAAAGRLGGAGWGRVPRPREL LSLSLVGR*GWRPQEQDQLFPH LRRPVGTRSESTWGNRAGAAT W/RAATPSPWRT*NGTKSKQW TASGLWQKGDGWD*GSGKPPL PLSPVAGQRLVPVC
14317	44685	A	14403	1150	1319	PRRLPTACTP*RS/CSRYWMVP KSPRMTMMMWTKLARMGAQ W*PRKSNACLSRAASS
14318	44686	A	14404	34	304	LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPRRAPPPAPRRVPST TQ/EARRSAASLLSPARPAHRD GTNNSRRATLRAVTLTARVRG F

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14319	44687	A	14405	1	360	SSLSYLPAGQGS GPAARHA*ASHPLHGLLCGSPSPNEHRPLIQGAQSH*PPKG*GVRAHGVGLA GRSTCSP/ECGIH*VKPAGLLSFLGPRCFYEL*QSPRRSAAASLLSP ARSRAHRE
14320	44688	B	14406	80	1166	
14321	44689	C	14407	1	543	
14322	44690	B	14408	1	930	
14323	44691	B	14409	1	1473	
14324	44692	A	14410	388	606	
14325	44693	A	14411	1	798	
14326	44694	A	14412	687	832	
14327	44695	B	14413	1	1218	
14328	44696	B	14414	1	642	
14329	44697	B	14415	1	807	
14330	44698	A	14416	554	724	
14331	44699	A	14417	216	494	
14332	44700	A	14418	1	3408	
14333	44701	A	14419	330	858	VPSLDGQRGLELDTECLRVVYLQ SLS*T*RFSTSSPEQLDTECLRV HSQQLC*TQGADWCYKP*VGL QVELPASPAP/WLAFSPWVVN GTGRHGAGGGARRGGSGCTGA HGVGGRLRHGRLQVPSAPWVE GSCLSPSPIGPPFKRAHSVLQKG SSTLMVGTCASSPKVVPFHLLS
14334	44702	B	14420	182	1513	
14335	44703	B	14421	1	1608	
14336	44704	C	14422	1	1830	
14337	44705	A	14423	167	433	LPSRGAGLGTCSPPCLSLPPTPW APVRSEPPRRAPP/GSTVPSPIN HPRAEECERMARDWQAAPPA PVRDPLGEASWAEFFGSMPL
14338	44706	B	14424	32	352	
14339	44707	B	14425	103	451	
14340	44708	A	14426	158	921	LPSRWAGLGTCSPPCLSLPPTP WAPVRSEPPRRAPSPAPRPVP/ RPPKG*GVPAHGA GLAGSSTCS PDICRVC RSEGTPEKPL.YH*CVCTGSIKFIHQECYSPDMPSRLPIQ DIFAGLVTSIGTAIRYWFHYTLV AFAWLGVVPLTA WHQLLDLGS TLNPGCSHLVILKLTITSTKTLFP NKATFILVVLSDQKTLMEDPR MEDKWKEDRFSFNFSEALEITL GERHRPQTASVIPWFCSSRHVL NLGKINFEVD

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14341	44709	A	14427	242	515	IQSVHWCIIHKP*ARHRVLIGVFT IPELDIKVLHVPTRLRNPAFTH WILHRDCRCSCMPVLRHAPALL SPWVVNGTGRSRAGDSTHRGG SG
14342	44710	A	14428	759	988	TWPRKPLFPPRPLGL*WEGMLQ RSLTCPGDIFPILVISIWL LVY ANFGSWL*FLPRKWVFFIPVP NKFLIFI
14343	44711	A	14429	130	788	VLQLIKAVWTPTQEPSWLPV NPARELQVELPASAPCARTPQ LLGGRWDWAPWSRGWRSGFE ARAAQKPMEGVGGSGMAGCR SRALPHGKAAKARRAIEHSTGG LALLGDPVHSPQPLARVLSPLP RASRAGWLLRVRGPPSPRPGT PAGRQAPHAAPVPARASPTTP/ CRAERVGSSPGQPRKGLPQCRG EAEGLLKCHQSGSPGRGEELW HSR
14344	44712	A	14430	108	1686	ANRCPLPHPGTGAGRCGLGASA GRAEEAGV*GPLHEGLGYRPA GLFLRADTGHRTPGWGGGGGG AGGRGGAAPGPGVATRRFAG RRGCARHGAAVPAAVR/CCERL VLNVAGLRFETRARTLGRFPDT LLGDPARRGRFYDDARREYFFD RHRPSFDAVLYYYQSGGLRRLRP AHVPLDVLEEVAFYGLGAAA LARLREDEGCPVPPERPLPRRAF ARQLWLLFEFPESQAARVLAV VSVLVILVSIVVFCLETLPDFRD DRDGTGLAAAAAGPFPAPLN GSSQMPGNPPRLPFNDPFFVVE TLCICWFSELLVRLVCPKAI FFKNVMNLIDFVAILPYFVALG TELARQRGVGGQAMSLAILRVI RLVRVFRIFKLSRHSKGLQLGQ TLRASMRELGLLIFFLFIGVVLF SSAVYFAEVDVDSHFTSIPESF WWAVVTMTTVGYGDMAPVT VGGKIVGSLCAIAGVLTISLPVP VIVSNFSFYHRETEGEEAGMF SHVDMQPCGPLEGKANGGLVD
14345	44713	A	14431	1	427	
14346	44714	B	14432	8	323	

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14347	44715	A	14433	20	1050	FNLVYMSHVSDEGALSSESASAT AASWPPHGFQLHFVPGRPQVPI CLYLLGQKGTG*HMAPLLRQVT GSPIPPKTIPGRGIRNMKRNEKR RYKTLMADGWELHQELSLGRT SSLPPYKGPWPSPGFQKVSKG ANPVEIKRGVMLAVDAVIAEL KKQSKPVTKEEIAQVATISAN GDKEIGNIISDAMKKCGRKGIIT KISSVQSIVTALEIANAYCKPLV IIAGDIDGEALTILILNRLKVGL QVVAVKAPGFGDNRKNQLKDT VIATGGEVGEVTVIKDYAMLL KGKGNKSQIEKCVQEIIDQSDV TTSEYEKEKLSIEKLSDGVAVL KSHPWSECTKIYPLT
14348	44716	A	14434	3	764	TTATVLARSIAKEGFEEKSKGA NPVEIRRGVMLAVDAVIAELKK QSKPVTTPPEIAQVATISANGD KEIGNIISDAMKKVGRKGVITV KDGKTLNDELEIHIEGMMKFDGR YISHPFINTSKQKCGISRDAYV LLSEKKIS/SIQSIVPA/LEIAHAH RKPLVIIAEDVDGEALSTLVLN RLKVGLQVVAVKA/PGFGDNR KNQLKDMAIATGGAVFGEEGL TLNLEDVQPHDLGKVGEVIVTK DDAMLLKGKGDK
14349	44717	A	14435	1	3288	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPI GVAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWVVDLHIIHAEDTLLPF YLGEKDDVYAIKPTCWPLDI IPSCALHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGITNVVC
14350	44718	A	14436	2	422	

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14351	44719	A	14437	529	2484	WGINIIKKNKKAAPRAFVGRLE ECQPATENQRWQDLNVISLLK SFFRKLPEPLFTDEELPLAPSCF EEENGGRGGGSPRYRLEPMDT IFVKNVKEDGPAHRAGLRTGD RLVKVNGESVIGKTYSQVIALI QNSDDTLLELSIMPKDEDILQLPA ERESGGEASEPPRVVRPEPSTRA LEPPAEDRGDEVVLRQKPPPTGR KVQLTPARQMNLFGEDESPEPE ASGRGERLGRKVAPLATTEDSL ASIPFIDICVRPCAWLHALLDW MAQQRVLDMQGSIGMGVSW DRELEEKSEKGYDEPTSPSIDL QAKHVPASAVVSSAMNSAPVL GTPSSPTFTTLGRHYSDQCST SAHLNIFAGIFDISNDHLQVSTL ESNFTRIHLTHYTGGNFPAWLA WDAVPFSSDLLNLGVHVLETG AGTPFLGSACSSDGIASQMNTA GLPQIRDLPGHYETLKLFLVGHV LKTIAHSEKKNMEPRNLALV FGPTLVRTSEDNMTDMVTPHA *PLTRSWETLIQALQTGSSVTKR YKKGKENCGLTRSLRQCPTLST FLPNIWQDSAPWRPGVSGPVGD LKDSTTCSSAKSKGSWAPKKEP YAREMLAISFISAVKPAQEA GDAGAGQQHRRRLGAGGAQS LGRGPQRRGHQERS
14352	44720	B	14438	1	1473	
14353	44721	A	14439	5	694	VPDKWGWCLFMSRYLETAIRT AACAAAPRYLNPGRCSAARGPS SQSPRPWPWSGHKRTASPGWG GQSAASPMPSPSRWPASVGGPE FRLSETPSRPFITLGMK*GWQV HSWAPALFCSVMSFSPDTCCLC K*AHSQPCSPSPSTVILLRETSSN WDWQPEDLGAPKASASPPSTT RITRLRSSELQLRRLNPSDSCHR GFCFSFRCLLTPEHVLKPTVLRI QPGCKVA
14354	44722	A	14440	303	757	MAWKVSLRGRKVAGRAPSQLR WASPPSSGQSVKSLLLPPARRL CPGPGVPARCHHRI*GLPGRG WRGEWRRDTPNWEPPQPRSPS/ G/PNCA WSDGCPGAPRRPRAL *AGAAARAAAPARI*VPWRGSAG GCSNRRLLQVPAHE*TPTFIRYL

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14355	44723	A	14441	1	534	RHEDHSEPTFLISPSLLCFLLP PPLPRLTPAALLVPAVQRME PVLFLPAPGAAACRVWHPALPP PRQAAVSSSRPCYPCVARSAPA GRVRAAGVPAPPPSSPRLGRV GGRSRSPNVVFRVGAAPGPG L*ISPWTP/LNEAS*RQRCGPAS FAVYGGQEWPRPQWGPGRGP
14356	44724	B	14442	157	2143	
14357	44725	A	14443	258	4089	QLITCLSRPETGGKFEVDTRP VCPPSRARAASAAAIAAAAA TLTPPTMDSFDLALLQEWDL LCVYEPDRNALRRKERERNQ ETQDDGTFNSSYSLFSEPKT NKGDELSNRJQNTLGNVDEMK DFLTDRTNQSHLVGVKPGVPQ TPVKNIDEHFVADSRAQNQPSI CSTTTSPAAPVPQSKRGTMG WQKAGHPSPDGGQQRATQGS LRTLGDGVGRQQ/HSGQTSVQC GGGSPDGEATCHGGQ
14358	44726	B	14444	1	1326	
14359	44727	A	14445	453	710	SQHFGKPRQVDHLRPGV*DP GQHGETPSLLKIQKLTGRGGAC LW/QSLLRRLRQENRLNLGGG GCSEPGSCHCPPAWATERDSVS
14360	44728	B	14446	32	290	
14361	44729	A	14447	244	426	
14362	44730	A	14448	69	221	QWRFCGIERGERWGKD*EIGW LPCLCGKK*IWETFLFCTKKN SSALGSC
14363	44731	A	14449	27	220	AVILTAKICSFTPEPSKTTSPGG TNNRRATLRAVTLTVKVCST P*GSAASFLKSVRPRTHQ
14364	44732	A	14450	115	732	EPETRIDPLSWNSSQLPVAALH LPGMSSVAGQAICNLCCGLDL VSPSSLPALERTGPPWNRGPK GRGRLPSL/TVSQPSLVIPPTG KSEVNADRSPRAYCSNLGRYS GPGPPSLVIPPTGKSEVNADRS GPPAYCSNHFPSPALP**RSSMRS LSLQQTSAWTCRHFTSLKSR WRFPNLNSCLCTCRPNITWKP CLGACTL
14365	44733	A	14451	528	875	EHGYFGQTLGQKGCKSGKPPG GTLKTLVTLREPGRLQSP*TS WVSERLP*YP*GDTGENCPKLS FHLRLGPS*AG*RERPPQGL YLPPQAYRLMQGSFAFWPLFGY APSPQR

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14366	44734	A	14452	2788	3414	ACFSYIAFWRIINTSTANLSKES LTSTTSRSWVINVIVICTDWL FYKWLKFNFIYFYMIFFNQIT FHSMGSCAARASPTSTPCSTA PSPIDHPRAEESSTRRTGRQL HLQPAKICSFTPEPSKTTSPGG TNNISALP*EL*HSPRRSAAL QFRTR*YPYRYSQSGPGSHF*L PLPLPSSIIHDHF*LFHLQHTFQS HALLP
14367	44735	A	14453	662	1338	VLQLIKAVVWTRPLGGRWDW APWSRRWCSGRLRPHRNQWS GWEAQAWGLQVPEPCPAGRQL RPGEKSSTA PVCTSCCRTRSTA GPTGCPSTRDPTLSASPS*TST TSLATATASASMWAGSCTSIST RGSASLVHQALTWPGSGPASPR KRVTGSHFVA*AGVRWRAHRS LPQTGPK*SSHFLPSGWNRYR HSNHPISQSFPHLSPLSQNH CHHGPFMS
14368	44736	A	14454	3	415	DFLLFSEILPASQASAILPALPA SHRCPCLLDVPLPPEVPGPARLP VAAASVWRPVQHLSSLGRWA GPT*DRTESRETNAEVEADLPP LYAHGRLEPTAGPSGASAVLST SSEYCPGPHPKMGHRRVTSCLS TCQS
14369	44737	A	14455	659	818	
14370	44738	A	14456	2	710	
14371	44739	A	14457	349	493	SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGGLHDLKIVVL
14372	44740	B	14458	1	1338	
14373	44741	A	14459	83	426	
14374	44742	A	14460	93	345	APALCLQILLDCXSVNRNRSF RPREVGIIQYKKGGAAGKGG TGNA PGFLLFKDS*KDPTPLPP PLLL*GQRDH*IQLHQE
14375	44743	A	14461	1	1302	
14376	44744	A	14462	1	1174	
14377	44745	A	14463	274	1428	
14378	44746	A	14464	411	627	HCLSHFQNTGPRGDVDFQQLA FPVLMADIRKEERSHLCSRSS TWILDKS*IQGSRLLSKEQGW GWGTSRK
14379	44747	B	14465	1	1553	
14380	44748	A	14466	226	449	SLQPDPI*CSGLRGSLLLV*PKSD
14381	44749	B	14467	1	2061	
14382	44750	B	14468	10	1099	

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14383	44751	A	14469	34	406	GGGFISLDTGSHHKSHPGGG*H ALGWVRPHLTNSPSPSQQPGNC GNPAWEC*GPHG/APSRWSCST PCRPSHPKVPAVRVAGPAGGCT PYRT/PTRRTPR*RPGPCAACDR PLHPHCGRPGGAYPR
14384	44752	A	14470	623	1671	VLRSSVSWLPTSMAMTVLAPM LRAMSAGRLLM*PPMSRCP SLGSHSGGR*PDS/GHAGAHVPPQ GAIFVDSHG*GGDICGHVEVRQ P/QGPQSAYPGRPDGCGG* RQTQ*TWRLGT*GPTQVPAPKSCS WPTPGPAASCGWRCAPPRTTLR *KSQWTCRPPGPRGPPPLMPL VLRCASSPWPRLAQGWCS P*APSPSGRSRCA GPRAWRKPS RRAHAAWQCGGAKRGGADSA GAGAPSTSCAYLATPRCAWGP HPPLGGAGLAA*GRAQPCSPAS APAGRG*APGPPGPQ*GCSR PVAGSARSASARRPSGRVRYGV HPPAGPATLTAGTLGCYVPRRP PGVPG
14385	44753	A	14471	32	972	QSGTFSTKNEGRFTTRDYYDGR GPRVGRCGTCVYVRYVHDRPH APPHERRRNDGNTQRTGNAR PGTAMPTATTDQPKGRSTRHK ETKRGRRTARNKGQNNPRK/RP RKDKRKQGSAGEGERGAGGKE KGQPRDTEAKGDRRTDFPPPNG /P*GQSKRGANIGGWFPPLGT PNPPLPGPQSAQVSGP*TPQM WMPGTGTGCCGGSQSGSPPPWCV SP*PVAEALFHSST/PAPRHPSP SSSPKHSHQSPSTPPP*ISLGGQ GPCRPPKRRPAPDQPPVRCPEPSC AYLATPRPTMRMQSACRGSAR SRASARRPSG
14386	44754	A	14472	1	3128	
14387	44755	B	14473	239	5474	
14388	44756	A	14474	542	781	PASIIIMTGSISHITILTRVNR LNASIKRHLRTDQWQIR/KSQDLSV CYIQETHFTCKDPHLKIKGWR KIYQVN*KQKKK

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14389	44757	A	14475	724	1340	QLTLQGRRVAPR*PSRVALEQE/ CGYNALLRYEGFENDSGLDFW CNICGSDIHPVGWCAASGKPLV PPRTIQHKYTNWKAFLVKRLTG AKTLPPDFSQKVSESMQYPFKP CMRVEVVDKRHLCTRVAVVE SVIGGRLRLVYEESEDRTDDFW CHMHSPLHHIGWSRIGHRFK RSDITKKQDGHFDTPHLFAKV RSFYKNPHL
14390	44758	A	14476	1822	2226	KRLFTNRTTRITPFVAINSHHHHH HHITINTIITTTTINSHHHHHY YHHHHHHHHHHQHHTTTTNTTT TNTTTTNNNTTTTITTTTNTTT TTSINSHHHHHNQCHHHHHH HHHH/HHHHHQYHHHHH*HYQ \\HHHHHHYYHHHHHHHHHHQ/ HHHHHHQHNNQHNNHHQQQH DHHHHYHHHHQHNNHHQHYQ/H HHHHHHNQCHHHHHHHHHHHQH HHDPHHHHQH*HSHQH
14391	44759	A	14477	232	625	EGCCCIAMVQKYSQPVRYVK YPFELIMALRKRYPRCCVTC* TGGAQQVGFRFLDPLSLCTP* CLWRTSSNF*KAAGCSGSR QSHHFGILPQPTAPKPWSSPLHI TKPQTLGQRDPGPRTRKRSK
14392	44760	A	14478	1	808	MPKTTACNVHTVTWASCENAD SDSTGLRHHDSCEDPASPGRS LCLVPHPTPAVRGGRPAGGRC PAVPAEGPWRHLQQAQEGKKR LAGGLERLENPVRRALPQGA QGHRAEPTEARPHAPEIRRAG AAAEARLESQPVGASAAAA SAASARIPYLVAVPAAGPPRRH CRRHRRGPGTSSGPRTALIRPAT ARARAGIVSEPTAPGATRARP WRQGSHPVAPSAP*LLRGPSIP WQIRPMPCTISHQTCSERRPSG RWQMPGSACRRSLETSSAGAG RAQEAGGRLGETSGESG/RAGL YLKELRAIVLNQQLVVRTQRQS IDELERRLNELSA*NRSLWEHP QLPQAQPPPGFLT*PSPLPALL GTAAATAAGAEHLQDHDGQRS SARPLPAPELASFQNEQLLAQ PEPDPGGRAHTTQSPHQHPGTL GVKANKEKKGPPGCCAAPGTP LQESPAAPSARES

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14393	44761	A	14479	1	831	MIRYFGDYWTQALLTLIPGDPK HPRGPPVKVGYYGGQGYINSL ALCHNFIWRELNRFSLLQDVPL VRYIDNIMLIGSIKFLGVQWCG ACRDIPSKDPADPMVLEVSAD RDAVWSIWQALIDESQQRPLGF WSKSLPSSADNYSPIERQLLAY YWALVETERSTMGHQTMLPE LPVMNWVLSDPSSHK/ANGLA GWSGTGKKHDWKIGDKIEWRR GMWMDLSEWSK/D/VKIFVSHV SAHQRVTSAAEEFNQVDRMT RSMDDTQPLYPTPIVIAQWAHE
14394	44762	B	14480	56	3476	
14395	44763	A	14481	3	591	DPADPMVLEVSEADRDA/VPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLTM GHQVTMRPELPINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQKWT VALQPLSGTSLQDSSEKSSQW
14396	44764	A	14482	1	1275	MEKNDIDQSRRRKVVEMNENV QLVRYGEQASDLKATKFKSPS EVKHIRFIQAFIGSKLLMRPW TTVTQILSLKSAKIALSESLIPC RKRAEFVEKQTQAFIMQVSD QQKVHAQPSQVSTVKVKALIG KEWDPATWNGDVWEGPDEAG DTEFVNSDEAFLPEATAFPSPEV GNDQTVWGLDGTSELMLIPG DPKYRGRPPVKVGA YGGQVIN RGLAQIQLSMDPVGHRTRPVVS SPLPECIIGTDILSSRNPHIGSLT DITLVHYIDDIMLIGSSEQEVTIT LDLLVQAVQAALPVGPYDPA DPMELKVSVADRDAVWSLWQ APIVTMRPERPIMNWVLSDPSS HKVGAQQHSIIKWKWYIRDW ARSGPEGTNHSRRVCS/LPQVQ APSA*ATARRGGQAASGCCLF WSTCFNSFDV
14397	44765	A	14483	604	1760	NSWCRWFNFRY*YPTFYWES* NT*IPLEWFG*NHDASCP*TL SKSFSFETRTGSPCSSSLQTAYC GTLWIVQGV
14398	44766	A	14484	2710	3060	
14399	44767	A	14485	3	227	
14400	44768	A	14486	3	266	
14401	44769	A	14487	2	564	

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14402	44770	A	14488	2	503	FFFFLPIGFWRQHIPRLSVLLQHI Y*VT*NAASFEWGPEQEAL*Q VQAVVQVALPLGPYPADPML LEVSVADKDAGCTRLAQAPIGE SQWRSLGFRSKALRSSAENYSS FERQLLACYWALVETECLTLG HQVTI*PELPIMNWVLSDPSSHK VGHEQQHSIIKWK
14403	44771	A	14489	2	469	
14404	44772	A	14490	1	633	MTVDYRKFNQVVTMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAFLPQ GYINFALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTDLLIHKRSKEAHTAASRI VSCLPEQKSHEQTL.PWEQVPSS GDIKEYFPNAFVLLTTASLQGG DNTSQLTLTWKAPEDIKMSKT DADADEEIEALRG
14405	44773	A	14491	1	518	MTVDYCKLNQVVIPIAAVSD VVSLLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQVTFTVLPPQWYINSPALCHNL IRRLDLCFSLPLDITLVHYIDD MLIGSTIKWVVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKH EWKTGDKGIRGRG
14406	44774	C	14492	33	932	
14407	44775	B	14493	27	2457	

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14408	44776	A	14494	332	2158	RGYVFCSSWKKTGDS/WRMTVD YCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQQQYTF TVLPQWYINSPALCHNLIRDDL DCFSLPLDITLVHYIDDIMLIGP RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVFLDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTTPVISQWPHEQCCHG GRDGGYAWAQCRLLPLTKAD LNTATAKRPICQQRPITLSPQY GTIPQGDQPATWWVVDYMG LPSWKGQRVLTGIDTYSYG AYPACNASAKTAICGLTECLH HHDIPIHSIADQGTFFMAKEVR QWAHDHGIHWSYHVSHHPEA AGLIEWWNGLLKSQLQCQLGD NTWQGWGKVLQKVYALNQH PIYGTVSPIAKIHRSRNQGLEVA PLTITPRDPLAKFLPPFATLQS AGLEVLVPEEGTLPFGDTMPL NWKRLRPPRHFGLLPLNQQA KKGVTVLAVGTDLDYKDEITL LLHNGGKEEYAWNTGDPLGLL LILPCPMIKVNGKLQQLKPEAL VPKGVVFPFGDTTMLSLSWKL RLPSGHVGLLMPLSQVQKGV
14409	44777	A	14495	1	3187	MAEGKEEQVLSYTDGSRQREN EEDAKAETPKTIRSHETYSLPR EWYEGNRPHDSITSQWVPPTTR GNYGSTIQDEIWDHSGHYVRP VPVPRSLNSDISYFVGVGKQAV FFVQGSARMISKPADSQDVHEL VLSKEDFEKKEKNKEIYSGYI RNRKDDYDNHTGIDLVGTHIATI KGSNEEDTDPLFIGKVRTLEFP FVNGSAEIMLMPNSQQHKTE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP
14410	44778	A	14496	266	467	
14411	44779	B	14497	152	1245	

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14412	44780	A	14498	1	1445	MLRAAAGGQGLAAAGMGLCA RPAGGSQPLPRERMKGNRACLP LPPAVALTKGREKPDAGHQGR STQMMRESERGPCTHWTEERP GRQLKILLQKQMRQNTLMAFQ VSWDGRNKEIGRTFPHTAPHT QQLIFAMKIKRTGTVPEPWGLF ETGQRIRPIQAAGL*LSSSSTTC VALAPLLTMHVKSALLSAP/Q MGALSTITSITTRRQIPAESHF PAARFHLAPHSPITLPPCCGP SESAVTLCFAKGKTAQDAAV PTTSLTAAGHLAPRS*SSWSRM PVKVRRAADSLPETSAAHPLT H*SWLPASWGPASRALPGSEW VLKPVWQ/AITGPVSQITSSPGIP KPIGPLQA*GSAHPQALGFSVL QIPLSNSPTSPMTPLPRPKISNS SLPSQ/PPQALFPNRWNTSSSPV HVITSAAQ/PRTPREWPAVSFYR TTATTASLPHLWAPPQEN*QTS PAQNGSTLPCMSQA TFHFPS
14413	44781	A	14499	44	455	HLNRNR/PSQITPHIYNHLIFDK /PLFNIWWENWLAICRKLKLD PFLTPTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/TGKDFM TKTPKAMATKAKIDIWLIKLL SFCTAKEITIRVNRLPT*WEKIF AIYP
14414	44782	A	14500	1	346	
14415	44783	A	14501	1926	2448	DFIAVITTRKQLTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKHKMKKCS SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRCRRGCCGIGTLLH CWWDCKLVPCLCKSMWRFLR DL/DPAILLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP

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14416	44784	A	14502	1	2142	MHILDAEKAFDKIQPFMLKTL NKLGDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFIATIKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DPIKLPMTFFTELEKTTLKEIW NQKRACTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSIYHN LIFYKPKDNKKWGNDSLFNKW CWENWLAICRKLKLDPLTPYT KIHSRWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVILKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELQIYRKKTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCCSSSLVIREMQIKTMM
14417	44785	A	14503	209	3816	QGRPTFRFKYREHHKDTFREE QLQDT*SSDSPKLK*RKCC*GQ PERKVKLPTKGSPSD*KRISRO/ KTLQARRQSWFFEKINKIDRPQ ARLIKKREKNQIDTIKNDKGD ITTDPTIEQITIREYYKHLVANK LENLEEMDKFLDTYTLPLNLQGE EVESVNRPTGSEIEAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLKLFLQPIEGILPNSFYEASII LIPKPGRDTTKGNFRPISLMNI DAKIL

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14418	44786	A	14504	1	2877	MENDFDELREEGFRQSNYSRLR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERVSAAME DEMNMKGEGKFREKRIKRNE QSLQEIWYVVRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPRQYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTITSEYYKHLVTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRNPITGAE
14419	44787	A	14505	1	2347	MELKTKARELHDECTSLSSRF QLEERVSVMEDEMNMNLPK KSPGPDGFTAIFYQRYKEELVP FLCLKFSIEKEGILPNSFYEPSII LIAKPGRDTTKENFRPISLMNI NAKILNKMLANQIQQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIIISDAEKAF DKIQQHFMKLKTLNKLVLVLA RAIRQEKEIKGLQKEEVKVS FADDMIVYLENPTVSAQNLLKL IGNFSKVSQYKINVQKSQAFLY TNNRQTERQIMSELPFTIAKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWGDLSLFNKWCWENWL AICRKVKLDPFLTPTKMNRSR WIKDLNVRPKTIKLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAACKHMKKC SSSLAIREMQIKTTMRVHLTPV RMAIHKSGNNRKIQ/GGIWCD RIL*R*TTCTRVAKIEQSL*RR/W KRLQRTLSIPVLDAV*PPMF*AS
14420	44788	B	14506	1	2265	
14421	44789	A	14507	1	2832	
14422	44790	A	14508	1	2109	
14423	44791	A	14509	1	2757	
14424	44792	A	14510	1	2304	

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14425	44793	A	14511	I	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFPSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRKLNLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELEIETQKTQVKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHLNANKLENLEEM DKFLDITYLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAIFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFTELKKTTLNFIWNQK IRAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLNFNKC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFSTAKE TTNRVNRQPTKWEKIFATYSSD
14426	44794	B	14512	I	2337	

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14427	44795	A	14513	1	1544	HINRAKDKNHMIISIDAFAED KIQQHFMLKTLNKLGDGTYFR KSINVIQHINRAKDKNHMIISID AEKAFDKIQQHFMLKTLNKLGI DGTYFRKSIN/DNPAYKQSQRQ KPLIISIDAFAEDKIQQPFMLK TLNKLONHIVYLENPIVSAPNLL KLISNFSKVSQYKINVKQSQA LYTNNSQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTKKWNIPCSWVG RINIVKMAILRKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA PVAKAILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI GQWNRTEPSEITPHVYNYLIFD KPEKTKQWGWKDSL FNKWCWE NWLAI CRKLKLD PFLTPYTKIN SRWIKDLNVRPKTIKLTLEENLGI TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTWEKTFATYSSDKG LISRIYNELKLIYKKTNPIK WAKDMNRHFSKEDIYAAKKH MKKCSSLAIREMQIKTTVRYH LTPVRMAIHKSGNN
14428	44796	B	14514	110	2153	
14429	44797	A	14515	1	3210	MVKGSIQEEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTROKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDLTLSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
14430	44798	A	14516	3	2820	ENKDDTTYQNLWDFAKAVCRG KFIALNAHKRKQERSKIDLTLS QLKELEKQEQTHSKASRRQEIT KIRAELEIETQKSLQKINESRS WFFERINNDRPLARLIKKKREK NQIDTIKNDKGDITDPTIEQTTI REYYKHLIYANKLKNLEEMDKF LDYTYLPRLNQEEVESLNRPIG SEIVTIINSLPTKSPGPDGFTAE FYQRYKEELVPFLKLFQSIEKE GILPNSFYEASILPKFGRDITK KENFR

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14431	44799	A	14517	687	2274	LRDCKRINQHPVKTDQSAFCM/APIMQDVVLEVLARAIQKEIKIGIQLGKEEVKLSLFADDMIVYLENPIVSAQNLLKLSINFSKVSQYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLTRDVKDLDFKENYKPLLKEITEDT NKWKNIPCSWVGRIINIVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLFKFIWNQKRARMASILSQ KNAAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNILIFDKPDKNKQW GKDSL FNK GWENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKLEENLDITQDIGMGK DFMKSTPKAMATKAKIDKWDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAACKHMKRCSSSLAIRE IQIKTTMRYYHLTPVRMAIHKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMQRKN TK TLI
14432	44800	B	14518	1	3192	
14433	44801	A	14519	1	2814	
14434	44802	A	14520	1	3144	MGDFNTPLSTLDRSSQKVNK DTQELNSTLHHADLIDYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRICKLTQNRSTTWKLN NLLNDYVWHNKMKAIEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKKQKQCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELEIETQKTLQKINES RSWFLEIRINKIDRPLARLIKKKR EKNQIDVIKNDK

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14435	44803	A	14521	1	2616	TTYQNLWDAFKA VCRGKFIAL NVHRRKQERSKIDTLTSQLKEL EKQEQTTHSKASRRQEITKIRAEI KEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDAI KNDKGDITNPTIEIQTITIREYYK HLYANKLENLEEMHKFLDTYT LPRLNQEEVESLNRPIGAEIVA IINSIPTKKSPGPDGFTGEFYQR YKEELVPFL/KLQFQIEKEGIM NIDAKILNKILANRIQQHIKKLI HHIQVGFIPGRQGFENICKSIN VIQHINRAKDKNHMHSIDA EKA FDKIQLFMLKTLNKL GIDGT FKIIRAIYDKPTANILNGKKLEA FPLKTGTGQCPLSPLFNIVLE VLARAIQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSQYKINVQKSO AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIVNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTA WYWYQNRD IDQWNRTPQSEITPHIYNILFD KPDKNQWQKGSFLFNKWCWE NWLAI CRKLKLDPLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGMDFM SKTPKAMAT KDKIDKWDLIKLSFCTAKETT

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14436	44804	A	14522	782	3024	SKTVPTGNSLEPTQNCWLQQW LPQDIEIEKQEQT/HSKASRRQEI TKIGAELEEIEETQKTLQKINESR SWFFEKINKSDRPLARLIKKKR EKNQIDAINKNDKGDITTDPTIEQ TTIREYCKHLYANKLENLEEMN KFLDTYTLPRLNQEEVESLNRPI TGSEIAIINSLPTKKSPGPDGFT AEFYQRYKEELHINRRTKDKNH MIISIDAEKAFDKIQRFMLKTL NKLVLVLEVLARAIQKEIKGVQ LGKEEVKLSLFADDMIVYLENP IVSAQNLLNLISNFSKVSQYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNERKEDTNKWK NIPCSWVERINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIKASILSQKNKAG GITLPDFKLYYKATVTKTAWYS YQNRDIDQWRNTEPSEILPRIYN YLIFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDPFLKP YTKIKSGWKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLSKFC TAKETTIRVNRQPTEREKIFATY SSDKGLISRIYKELQIYKKRTN NLIKKWVKDMNRHFSKEDVYA AKKHKMKCCSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRITI VLLPGSLIVRSFHVTLNAILLHP
14437	44805	A	14523	1	1701	
14438	44806	A	14524	1	4434	
14439	44807	A	14525	1	2913	MGGPAALCIAVVPGLDVVALC LEEGLSGSIATWACSPWRISQ THLTFRSSLAVAAIPEGLPIVVM VTLVLGVLRLMAKKRIVVKKLP VETLGCCSVLCSDKTGLTANE MTVTQLVTSGLRAEVSGVGY DGQGTVCLLPSKEVKEFSNVS VGKLVEAGCVANNAVIRKNAV MGQPTEGALMALAKDQEDY FMKGALVEEVIRYCTMYNNGGIP LPLTPQQRGAGPDTALPSAAS AFARMSAAERNDAFQG

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14440	44808	A	14526	1	3009	MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDGS AIKLELRKIKNLTONRSTTWKLN NLLNDYWVPNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14441	44809	A	14527	1	4800	MGDFNTPLSTLDRSTROKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRKIKNLQSRSTTWKLN NLLNDYWVNNEMKAEIKMFF ETKENKDDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
14442	44810	B	14528	1	2901	
14443	44811	A	14529	569	3443	RKH*TWKRTSSTSHHKNNPN* LEKQEQTHSKASRRQEITKIRAE LKEIETQKTVQKINESRSWFFER SNKIYRPLSLRIKKKREKNQIDT IKNDKGDITTDPTETIQTIREYY KHLANKLENLEEMDKFLDITY TLPRNLQEEIESLNRPIGTETIVT IINSLPTKKSPGPDGTAEFYQR YKEELVPFLKLFSIEKEGILP NSFYEASILIAPGRDITTKEN FRPISLMNIDAKILNKILAKRIQ
14444	44812	A	14530	3591	8157	TGTSQKKTfMQPKKHMKKCST ITGHQSNANQNHNIPSHTKLE WRSLKRSGNNRDVGNVVEAM YGDLPPIMLIGHSMGGAIAVH TASSNLVPSLLGLCMIDVVEGT AMDALNSMQNFLRGRPKTFKS LENAIEWRNKIDLSWADSIKNV AAASLACISGALPASAVTTSPD NKRMRNVLYKIERLLAESPNH VVAEAVIQRPNIPLQTRDTYE GLCQTLGSQPTLYQIPSLYCSYE TNSNAYLLLQPIRKEVI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, v=-possible nucleotide insertion)
14445	44813	A	14531	172	328	AVKTEPEMSQATKLSVVHEK KSQEGKPKHEPEKSLPKQASD TGSNDAHNIKAVSR*SHRQPSC LWFMKKNPKKESRKNTQSQKA YPSRHQIQEVTMLTI
14446	44814	A	14532	3	660	TSPDCWEGRSVDWPRPGPALS LHNCKLDLGIEGTLQPTTSPF* PTGTRAV/PTRRRSRQETQLNSE RTVSPGSR**EKRTSRAW/RSP QGPGPGHAGQVAGGTGPRIGS TRGD/TLQKCGKIQSVPLNCELI PI*/PSILKPKVLPSCPGIGASSV CPSD*VFFCTS*PWPVLLSYPLS MNFYRYHDHILKLLVQYTLVYL LLQFLQVLLKYLLSHPKQHS
14447	44815	A	14533	1	1086	MVDNDVPWPLVVAQEKQPD LCLSSKGYRPLALVQLDFHQVS VTSKIFILSGALRSLTGAATAD WTCRVLVIYPHDIMADSECNLS LVPSTRKIMKHLASEKIKTQ NFNYNVDECVSLLYHHKANKL EAAEARQECCELLRVASVSRHC W/RDPAHPHSCWPRC*APHCLG PARAPNARPAKPATTWNLRSSR APCAAPVPTQSWAGAPSGTAG AEPS*ECRPPENQARTAGSGVH AEACAPATCAPCGPGPCSGLP SSGRALFLL/CATLAIPC*V*LC FLATPPPCR*HVTAPSAGKCIW* PDA*VTK/PRDLCPVQVARDN GPRQVAQKKESSVVSWFGTFI SRVGDSPPPRAATL
14448	44816	A	14534	23	506	PDIDNIFEFGAKSKPYLTVDQ MMDFINLKQRPRLNEILYPPL KQEQQVQLIEKYEPNNSLARKG QISVDGFMRYLSGEENGVSPE KLDLNEDMSHPLSHYFINSSH TYLTGMNVLVLCYFSQSHQISP TSTFCSEAEV/WFSSISCVEPLR TLGFHH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
14449	44817	A	14535	341	1248	KNAFTSFLTSFPFGQISVDGFMR YLSGEENGVSPEKLDLNEDM SQPLCFMGIWGLFCWCFIAGQL AGNSSVEMYRQVLLSGCRCVE LDCWKGRATAEEEPVKILAY* IYMCSHF*EVIEAIAECAFKTL SLPTFLLLFLFSLSPKQQA KMAEYCRLLIGSSIFKEYAFHFY* LESGVPLPSPMDLMYKILV KNKKSHKSESGSGKKKLE SEQASNTYC*NGDMMICY* NLTEADTESDADSGNV/CLFY SYFQGTAGSEAMATEEMS NLVNFLLTPFFVLLLNSE RNKSFEMSSFVETKGL
14450	44818	A	14536	574	647	C*PGNM/HISGQHLVAGEKEAE SEDEEEEDMKLLGTPEGGSKFT QKKVKLADEDDDD/DDDADDD DDDDDDDDFDEETEEKAPV
14451	44819	A	14537	3	630	PGATHASAPPGVRLKCGSGPV HIIGQHLVAVEEDAQSQDEEEE DVKLLSISGKRSAPGGGSKVPQ KKVKLADEDDDDDDDEEDDD EDDDDDDDFDEEAEQQA PVKKSNRDTPAKNAQKSNQNGKDSK PSSTPRSKGGQESFKKQEKTPKTP KGPSSVEDIKAKMQASI/EKKG GSLPKVEAKFINVYVKNCSRMT DQEAHQDLWRWRRSL
14452	44820	A	14538	1	1971	
14453	44821	A	14539	316	1169	RVGGQSHGTQRISLCRHSVCSP LARQSPSNMK*VRTIEIQMAVS CYLKRWQYVDSGGLPKQGLR LPQTAEEELANLTVHRESHCAD IVSAVPCQAEPOQYEV/QFGR LRNFLIDSDSPHSHEVMPLLYPLF VCLHLSLVQNSPKSTVESFYSR FHGMFLQKASQKGVIEQLQTT QTIQDILSNFKLRAFLDNNYVV HLQEDSYNLIHLYLQSDSYTAL CKMFILLIHLDVQPAKTTD*QL YASGSSSRSENYYLEAPDMPSPI LQNDAALEVLQERIKQVKDGC PSLTTVCFYNT*QLLNTAEISPD SKLLAAGFDNSCIKLWSLQSRK LKSESCQVDMRSIHLACDILEE
14454	44822	A	14540	1	297	

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14455	44823	A	14541	2	1089	APLLGECRSGRGLASSRSRRRT TMTQSVVVQGKLRAGRDLVA AESSGHVSLMSYSLSFLSSGRS RLALREHAAVNQVPARRREPPR LSARSSSPYSFHLQSE*L*KKIH* LYFIFLSQAVLIDMEEGVVNEIL L*IRTNQIKK*MQGIFKIHILIFR AVGHKVFGLYQDQIIEKFQIL HNYILNHLCL*FLKTL*SSGTGSG LGTFLKLVLEDFPEVYRFVTSI YPSGEDDVITSPLVEYHLHPLF LIA SLPMFFPQKSLFDIISKIDLM VNSGKV/GGTTVKPKSL\VTSSS GALKIELHLKCIILKLIKFSF*C* LFSSARFEGSLNMDLNEISMNL VPFPSS*EIVSLKYVLYFN
14456	44824	A	14542	129	461	TCISGWHLFRASVTCPGIQTSPH NWHISDNSSLPNNIFVCWNLL GMTRNYIIFIEQPLKMNLWKIA TSKIRGKAFSDGISGNPQCNT FHVVEKRTGQLLPGRYYSKPF
14457	44825	A	14543	1	522	
14458	44826	A	14544	1	927	MEDLLTEARSPYWGRARAKIQ DSCWSVTSDPNAGSV DILAPLL LPSPSSYLPNFTCTSVVVTSHLH EAFDLGLFRGTGGSNCKTSRQV QLNNQKRKKKKSKSLPFHMSL QIQNYKTQEEP HAKPSSQQHQH SEHESIQTCLVFRSSMTYMH TL KLIREKGSIMLSSTQGECPNSTC RWPAEEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNLWKIATSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQT T*INPDKISIQKHDIHAYIEAD KRKRKHNAVIHTG*M/YQI/GTC RWPAEEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNLWKIATSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQT LNVKTMRMKTFMMIYYHLMN

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14459	44827	A	14545	1	882	MAEILTQVPDDMLKKKTPRVK SVWRSQRGSCTPLIGTTTLD TSHMSIRNMDRSHINVHTVRKP SADLPYFRTHEWAHTGGKPYD CEECGKSFISRSSIRRHIMHSG DGPYKCNFCGKALMCLSLYLIH KRTHTGEKPYECKQCGKAFSH SGSLRIHERTHTGEKPYECSECG KAFHSSTCLHAHKITHTGEKPY ECKQCGKAFVSFNSVRYHERT HTGEKPYECKQCGKAFRSASH LRTHGRTHTGEKPYECKQCGK AF*PRFQMT*RRKLPE*NQCG EVSUGHVHSLNRHHRADTGHKP YEQYEGQKPYKCTYCKKAFS YLPYFRTHEWAHTGGKPYDCE ECGKSFISRSSIRRHIMHSGDG PYKCNFCGKALMCLSLYLIHHR THTGEKPYECKQCGKAFSHSGS LRIHERTHTGEKPYECSECGKA FHSSTCLHAHKITHTGEKPYEC KQCGKAFVSFNSVRYHERTHT GEKPYECKQCGKAFRSASHLRT HGRTHTGEKPYECKQCGKAFG CASSVKIHERTHTGEKPCSSNTS
14460	44828	A	14546	3	395	SAEVGAAETTLTELRRTVQSL DLDSMRNLKASLENSLGILLHL ESELATRAEGQRQAQEYEA LNKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTT RRIVDGKVVSETNDTKVLRH
14461	44829	A	14547	2	1044	AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLLRASEVEGYS LPACAEPPVQSECLSHLSVWSL QHALSSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNGGGLA GMGGIQNEKETMQSLRDRLAS YLDVRVRGLETENWKLESQIEH LNVTRL*LETEIEALKKELLFM KKNNEEFAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRQA YDKLARKNREELDKYWSQIE ESTRVVTTQSAKVGAAMTLT ELRHRVQSLIEDSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV

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14462	44830	A	14548	1	1212	GP GTGIAGGLAGMGGIQNEKET MQSLNDR LASYLDVRSL ETE NRRLESKIREHLEKKGPQVRD WSHYFKIIEDLRAQIFANTVDN ARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKYDD TNITRLQLETEIEAL K*ELLFMK KTPEEEVKGLQAQIASSGLTVE VDAPKSDI AKIMADIRVAQY DELARKINRELDKYWSQQIEE STTVTTQSAEVGAAETITLTEL RRTVQVFGDSTWTSMRNLKA NLENSLGEVEARYALQMEQLA NGILLHLESQLGQTPTREARQ AQEYEA LLNLIKVKLAEIICHL TRPPSWKIGDFNLGDSLDER NSMQTIQKTTRRISWIGQSGV LRPIDTKVLEALSQQEASGTL LKQEANKKFQSFK
14463	44831	A	14549	1	2382	
14464	44832	A	14550	2	173	
14465	44833	C	14551	1	732	
14466	44834	A	14552	455	682	AWKRAVALGKSRPMGAVAFK RRMQPVAGPRAMQEKFPSSSS SLSIIPAF*YRLALSLAEPSSRW RARTGALMQL
14467	44835	A	14553	158	368	
14468	44836	A	14554	87	251	
14469	44837	A	14555	1	1026	
14470	44838	A	14556	201	578	
14471	44839	A	14557	336	767	AFVRAGSRFGGTPGARPDPA TRAPNPVGQSRHLRAASSRGRL FLRRTRDRKFPRRPLSRLLG A1/GCRWNQPRAAEKSFSAGAV LDFSPGLSCLPAVQSGSPAARH A*ASHPLHGLCCPSIPDEHHPL LHGAQSHRPPKG
14472	44840	A	14558	6	535	ARHRVLIGVFTIPELDILSTSPD SGAQLASPSDPAAGLQVELPAS PARCARIPQLGGRWDWAQTQ EPSWLHLVEPAPGLQVELPAS TPCACIPQLGDRWDWAPWSR GWCSLGR LGPHRSPWGWEEAE AWRAAGPEPCPTGRQLRLGEK SSAAPVGWHCWGTQYTLRSH WPGC
14473	44841	A	14559	375	638	
14474	44842	A	14560	92	514	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
14475	44843	A	14561	54	380	SCHHYCRIHRRCARFLAGP*LPS RGARLGTCSPPCVSLPPAPWAP VRPEPPRRAPPPAPQRPVPSITTQ GLRSAGARRGTGRQLHLQLRG SAASFLKSVRPRTHTQFRTHT
14476	44844	A	14562	531	773	
14477	44845	B	14563	92	1774	
14478	44846	A	14564	1	390	LHDLQLSKPLSDDTALTDGG/Q PLPARWWAQPGRLQRCARFLA GP*LPSR/WGRARDLQAMPEP PTPSVGSCAAQASPTSAAPCSM APSPIDHPRAWPVLCSCMLLS LFVASISSCSQHQPQMVGTMVC L
14479	44847	A	14565	165	545	SLHSKLCWWLQQLWVYDTCP CSVQDCRQRWASAGNQS*RLL VDPAPGLQVELPANPVPCARIP QPLGGRWD*APWSRGWCSSGR LGLHRSFWSGWEAQWRAAG PEPRPAGRQLGAMSKVETGT
14480	44848	A	14566	1	309	SACLAGRPIRGPRDLQAM PEPPTPSMGSCAARASPTSATPC STAPSPIHHSRAEECGHTALG/H GRQLHLQPRNLPQTINWRTTYS SFPATLNLDDGGG
14481	44849	B	14567	1	843	
14482	44850	A	14568	143	535	
14483	44851	A	14569	375	571	
14484	44852	B	14570	289	972	
14485	44853	A	14571	27	363	
14486	44854	A	14572	2	490	
14487	44855	A	14573	574	961	RLTLPDLRGSPPDTHQAQQITW ALI.PQGFADSPHYFSQAQISSSS ITYLGIHLHENTRALPADHV*LIS QTPISSTKQQLLSFLGMVRYFC LWIPSFTILTKPLY*FTKANLAD PTDPKSFPHSSFRSL
14488	44856	B	14574	182	1513	
14489	44857	A	14575	894	1305	QTQEPSWLHLVDPALGLQVELP ASPVPCARIPQLGG*WDWAP WSRGWCSSGRLGPHRSPWSGW EAQAWRAAGPEPCPAGRQLRP GQHPL/RHMNKSQALSLLIAQP LGINLLSWWPPKYNRVPVLI SGLLIPATF
14490	44858	A	14576	531	801	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
14491	44859	A	14577	441	783	RAPPPAPWRPVSTTQGLRSAG EQRGTGRQLHLASAAPVRDPRG EAIWAPESGRSAASILKPARPPA HREERTTPDAPP*EL*HSPRKS ASLREDPWLS*SQ*DQEPNTS GHTVSQDQSYYS*LEVSETKNP PIPDTL
14492	44860	A	14578	344	1632	FLAGPYLPSHGAGLGTCSLPCL SLPPTPWAPVRPEP/PPMSTTPCS TAPSPIDHPRAECERTAQDWQ AAPPAAPVWDPLGEASWAPES GTNISITPGNATFVTRVQQQAW FASCITGHDMSSLKTSVVVLR RQSEALLPANLTCNWQDSSAL ATLESALSQVRHKRFTFTLMVF TGSADIMATVSIADVVSITESVQ TTAFVDNLAKNICDELLQDM DEAGNQHSQQNNTRTENQTPH VLTHKWELNNENIRIQGGEHYI LGPVGGRDEKTLRLRTYCLKSQ EGADTKCRNKHNETQKQSKS LVYSSTLNPEKLLVCKRLSLEL TRPENTLRCNTNIGKLKAVAGG MSAASGIYLETDTQPYPLKQEL KEIKECVGKNSVVVVFLVRKK LSVSQYAFARCLDAKHSTSENV EIAKGLRIQSFEVKGQL

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14493	44861	A	14579	3	2233	NWLPSVSRCEQETHKIAANQSLT QRQMPLTSLYCDVVILPVSVGL ESLQSPYYRTSPCDPVSQFLIK ISASSLPVLSLWTKLNKNAQSVQ RDYRHDNKAHYFQKLVMTQE NLYVLLCDEELDAVSLEAVHQ QKMKNRQAHSSGCCQKVAN APRNEESSGQFRVIGNEKFEKG PCGVRQQIFEKVLLPNRTCEV TPRFNRNFDLIKDLKAAETLID FLVYEPKNQRRLVNRFRLPCKL LHNLGHPLKTDAAQSPRKPPGP SWMPSPGSKPPSHPLVSPHLNP QVWDTSPPSLATEHASLTISLKP NHPPYPAQSQYSIPQHALKGSKP VITRLLEHGLLKPINSYPNSPILP VQKLDKSYRLVQHLCLIQIVL PIHPMVPNPYTLSSIPFTTHYS VLDLKHAFITILYPSSQPLFAF TWTDPDTHQAQQITLAVLPQCF IDSPHYFSQAQISSSVTYLGIIL MKTHIGLGAVEQGVVLVGEAR AAQEPMEWVGSGM/CGLQVP SPAPWEGS*GPARNRAQIPVTIV PVLDFNPAPFHIPDTTPDHHDCI SLIHLTFTFPFHISFFVPVPLEHT WFIDGSSTRPNCHSPAKEYAI VSSTSIIEATALPRSTTSQQAKLI AYTDSKCAFHILHHHAVIWEER NFLTMQGASINAFLIKTLKDI LLPKEAGVIHCKGHQKASDPIT QDNAYADKVAKQLAFQLLSL
14494	44862	A	14580	1	642	SGTVPTTFVRTVIQAQGARTVI QQSLIGSLYIFRHCVRCOGIESV FVIIIWSRVGYDEKGFCLFTSVL GVWGHVTRKPCLLITWRTLKS RSGLE*PAGFSSSPGTSPQIRKQ KRGVPQHPVCDLPGRFRPRAGT PLAAQIQVPLPPCGHQE*NRR WAGSSALCPPLYLCARAGTGAV CRACEPAGV/AGWAWAWWAP HSEHAASAPGRQWGT
14495	44863	B	14581	393	549	
14496	44864	B	14582	1	591	
14497	44865	C	14583	226	828	
14498	44866	A	14584	1	1362	

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14499	44867	A	14585	1	585	MANVHQTMPLRLRLPDSFKP PEPKSNSQRVSTEAGTAGALTP QHVRHSSPASLQLGAVSPGTL TPTGVVSGPAATPTAQHFQSS FEIPDDVPLPAAREMAKTSSGQ RYFLNHIDQKTTQDDPRKTM SQMNVIANPPVQQNMNNS/PQS PQGGV/MGGSNSNQQRMRPQ QLQMEERLQLKQQ*LLQELALR
14500	44868	A	14586	345	1053	RWRLQNLSCSSCSGSGSEGAT CFARGRQSNLQSKIFPSNTD SRSTGYNSFDRQPNICFYKRQE TPHTGPIIPVPEGRPYMPG*CG A*SPGPFASRN*SEKN*SYKCSL HTAFNVIFSSVI**RYCTRQWHI VKCLDSFCDPFLISDELRRASTD AGTAGALTPQHVRHSSPASLQ LGAVSPGTLTPTGVVSGPAATP TAQHLRQSSFEIPDDVPLPTSW GEAKTSSGSKIPIF
14501	44869	B	14587	607	1185	

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14502	44870	A	14588	1	2142	MIILDAEKAFDKIQPFMLKTL NKLIGDGYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGGP LSPLLFNIVLEVLAAQIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRKYLGQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWGRINIMKMAFPR WELNNENTWTQEGEHHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRKYLGQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTLSSKNAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTASEVTSHIYNH LIFYKPKDNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKLTLEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVILKKSFCTA KETTRVSRQPTIEWEKIFAIPPS DKGLISRIYKELQIYRKKTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
14503	44871	B	14589	1	1647	
14504	44872	B	14590	1	2025	
14505	44873	B	14591	4	2121	
14506	44874	A	14592	2	1879	
14507	44875	A	14593	1	2130	
14508	44876	A	14594	1	3018	
14509	44877	B	14595	1	3171	

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14510	44878	A	14596	1	2700	MEKKQSRKKTGNSKNQASPPPP KECSSLQATEHSWMENDFDEL REQGFRRSNYSELKEEVRTHGK EVKNLEKRLDEWLTRITNAEKS LKDLMEKKTMARELLDECINLS SQFDQLEERVSVSMENQMNEMK PNLRLIGVPESDGENGTKLENT LQDIIQENFPNLARQANIQIEIQ RMSQRYSSRAIPRHIIVRFTKV EMKEKMLRAAREKGRVTLKG KPIRLKADLSVETLQARREWGP IFNILEKNFQPRTSYPGKLSFIS EGEMKSFTDKQKLRVYVTTTRP ALKELLKEALNMERNRNYQPL EKQIQTITIREYYKHL YANELEN LEEMDKFFDITYTLPRLNQEEVE SLNRPITGFEIEAIINSLP/TKKSP EPGGFTAEFYQRIEKEGILPNSF YEASIIILMLKPGRDTTKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHQDQVGFIPGMQGWFNIR KSINIIQHINRTNDKNHIIISIDA EKAFYKIQQPFMLKTLNKLGD GSYLKIIRAIYDKPTANIILNGQ KLEAFPLKTGTGRQCPLSPLLF NLVLEVLARAIHQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIA SAQNLLKLKGNFSKVSQYKINV QKSQAFLYTKNRQTESQIMSEL PFTIASKRIKYLGIQLTRDMKDL FKENYKPLLNEIKEDTNKWKNI PCSWEGRISILQMAILPEVIYRF
14511	44879	A	14597	1	2310	
14512	44880	A	14598	1	1305	
14513	44881	A	14599	1	2148	
14514	44882	B	14600	1	777	
14515	44883	A	14601	2	2971	
14516	44884	A	14602	1	3810	

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14517	44885	A	14603	1	1773	MNIGAKIINKILANQIQGHIRKLI HHQVGFIPGMQGWFNICKSIN VIQHINRTKDKNHMHSIDA CDKIQQRFMLKTLNKLGDGKY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKDIQLGKEEV KLSLCADKMIVYLENPIVSAQN LLKLISNFSKVSQYKINQKQSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLQIHQTRDVKDLFKEN YKPLLKEIKEDTNKINIPSCV RINIVKMAILPKELEKTTLKFIW NQKRARITKSILSQKNKAGSIM LPDFNLYYKATVSKTAWY QNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNQWGDLSFNK WCWENWLAICRKLKLDPLTL YTKINSRWIKDLNVSPKTIKLE ENLDITIQDIGMGKDFMSKTAK AMAAKAMSTKAKFGKWDLIK LKSFTAKETTIRVNRISYASS STSLQAFSRKILNCSKRFKIAQ MCKLVELRPQDMHITSRGSGNC SEARTLLCDFSAGRTSVNHGRI WRQIREAGAADPEIGLEVCNKN PTSFTLFYFLSYTTG
14518	44886	B	14604	1	2070	
14519	44887	B	14605	1	3190	
14520	44888	A	14606	1	3370	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14521	44889	A	14607	569	3030	RKH*TWKRTSSTSHHKNMNP* LEKQEQTTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKKREKNQI DTIKNDEGDITTHPTIHTIIREY YKHLANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLK1.FQSIEKEGILPNSF YEASIIIPKPGRDITTKENFRPI SLLNINAKILNKILANRIQHHK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIISID AEKAFDKIQPFMLKTLNKLGI DGTYYHKIIRANYDKPTANIILNG QKLEAFPLKTGTQGCPLSPLL FNIVLEVLAIRQEKETEGIQLL GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKIN VQKSQVFLYTDNRQTESQIISEL PFTIASKRIKYLGIQLTRYVVDL FKER/YNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIVNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPKDNKQWGNDSLFNKC WENWLAICKKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLEEN LGNNIQDIGMGKDFTSKTPKA MATKDKIDKWDLMLKLSFCTA
14522	44890	A	14608	1	2742	
14523	44891	A	14609	1	3828	
14524	44892	A	14610	1	2667	
14525	44893	A	14611	1	2325	
14526	44894	A	14612	1	3057	

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14527	44895	A	14613	603	2973	DNTARGETIRQQHLLFTNIRCSA ASAADTQANRVWSGPPANSNR PAAARVLTVRRTKNKQKGHPH QNPICTSPPSKTKETQTTIREYY KHLIYANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRTESDIE AIINSLPTKKSPGPDGFTAIFYQ RYKEELVPFLKLFQSIEKEGIL PNSFYEASIIIPKLRDRTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKHHGGVGFIPGMQGW FNIRKSINVIQIHINRTNDKNHMI VSIDAFAFDKIQQPFMLKTLN KLGDGPYLKIIIRAIYDKLTANII LNGQKLEAFPLKTGTROGCLLS PLLFNIVLEVLARAIQEKEIKGI QLGKEEVKLCLEFADDMIVYLE NPIVSAQNLLKLISNFSKVSQYK INVQKSAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTGDV KDFFKENYKPLLNEIKEDTDKW KNIPCSRVRINIMKMAILPKVI YRFNAIPKLPMTFFTELEKTTL KFIWNQKRARIKASILSQKNKA GGITLPDFKLYYKATVTKTACH RVGRAQQHSISKWKWYIHDWS QVGPEGTNDSARYPDTTQKWT AAALQPLSRTSLKDSHEGKSSQ WAELEAVHLVLRFAWKEKWP DVQLYTDSWAVASGLAGWSG TWWKHDWKIGDKEIWGRATPV IAQWAHEQQRGHGGRDGDYAW
14528	44896	B	14614	1	3105	
14529	44897	A	14615	1	3654	

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14530	44898	A	14616	735	2839	RSFPRSFPFLLSRYLRHIMV FSVLPFGLQNP KYLLSGSLQEK FRTPGINSHKTLDPNRVLIKVR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITDATEIQTITREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPTGSEIAIINSL PTKRSPGPDGFTAIFYQTYKEE LVPFPLKLFQSTEKEGILPNSFY EASIIIPKGRDRTTKKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHQDQVGFIPGMQGWFNKRK SINVQHINRTNDKNHMIISIDAE KAFDKIQQPFMLKTLNKLIGDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCPSPLLFNI VLEVLAARVRQEKEIEGIGLQK EEVKLSLFADDMIVYLENPIVS AQNLKKLISNFSKVSQYKINIQK SQAFLYTNNRQTESQIMSELPFT TASKKIKYLGIGLQTRDVKDLFK ENYKPLLNEIKEDTNKWNIPC SWVGRINIMKMAILPKVICRFN AIPKLPMPFFTELETTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITHIYNYLI FDKPEKMSIIDTGGWYEA PVSS FFKEGLCRTGTENQVNRQPPAA SPFKVYVVSCTGSLHPRPHYFLE
14531	44899	A	14617	1	2250	
14532	44900	A	14618	1	2870	MKAIEKVFFETNENKDDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDTSLQKLEKEQEQT HSKASRRQEITKIRAELEIQTQ KTLQKINESRSWFFERINKIDRS LARLIKKREKNQIDTIKNDKG DITDPTEIQTITREYYKHLYAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTGAEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK

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14533	44901	A	14619	248	2623	RQWAGVVGRCSHLASVWSSNT SETGAIRSSSTEVDAPDDSMMLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAIFYQRCKEELVPFL KLFQSI/EKEGILPNLFDEASILI PKRGRDITTKENFRPISLMNID AKILNKILANRNQQHKKLIHH DQVGFIPIGMQGWFNICKSINVI QHINRTKDKNHMIISIDAFAKAF DKIQQPFMLKTLNKLGDGTYL KIIIRAIYDKPTANIILNGQKLEAF PLKTGTROGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKWKINPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIVNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWYWYQNRDIDQ WNRTEPSEITPHIYNYLIFDKPE KNKQWKGKDSL FNKCWENWL AICRKLKLDPFLTPYTKIHPRWI KDLNVRPKTIKTEENLGNTIQ DIGMGKDFMSKTPKAMAACA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKKTNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPLAIREMQIKTTMRYHL
14534	44902	A	14620	1	3253	MGDFNTPLSLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFPSAPHITYSKIDHIV GSKALLSKWKRTIHTNYLSDH SAIKLELRILNLTQSRSTTWKLN NLLNDYVWHNEMKAIEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQIDTIKNDK
14535	44903	B	14621	1	2758	
14536	44904	A	14622	1	5178	

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14537	44905	A	14623	1	3382	MGDFNTPLSTLDRSTRQKVNK DTQEFNSALYQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCERTEIITNLYSDHS AMKLELRKIKNTQNCSTTWKL NNLLNDYVWHNEMKAEIKM FFETNENKDTTNQNLWDAFKA VCRGKFIALNAHKRKQERSKID TLTSQLEKELEKQEQTHSKASRR QEITKIRAELEKIEIETQKTLQKIN ESRSWFFERINKIDRPLARLIKK KREKNQIDTIKNDK
14538	44906	A	14624	965	4091	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEYTFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITN YLSHSAIKLELRKIKNLNQRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKELEKQEQTHSKA SRRQEITKIRAELEKIEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID
14539	44907	A	14625	3	3229	
14540	44908	B	14626	1	2791	
14541	44909	A	14627	1	3158	MVKGSIQEQEELTILNIYAPNTG APRFIKQLSDLRDLDSHTLIM GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNLYSDHSAI KLELRKIKNTQSRSTTWKLNNL LLNDYWRKQERSKDTTLTSQLE KELEKQEQTHSKASRRQEITKIR AELEKIEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKKEKNQID TIKNDKGD
14542	44910	B	14628	1	7849	
14543	44911	A	14629	1	3985	MENDFDELREEGFRSSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRSLRSRCDQLEERSAM EDEMNMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLARQANVQIQIRMPQRYSS RRATPRHIIVRFTKVEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDYRTLHPKSTEYTF FSAPHHTYSKID

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14544	44912	B	14630	64	5735	
14545	44913	B	14631	891	6894	
14546	44914	A	14632	33	476	
14547	44915	A	14633	1	360	GQGEPKQLGRHPGVLRPHVVS AKTGDAC/IWQVRNLFPERPK VQWKEGCA/LQSGNSQESVTEQ GSKVSA YLSSPLT LSKADYEK HKLYACEVTHQGLSSPVTKSFN RGEIIEGEVPPCI
14548	44916	A	14634	40	508	LPGECHRAQQGQRLQPQLLG LLMLWVPGSGGEIVMTQTPLSS SVTLGQPASISCRSSQSLVHSDG NTYLTWLQRRPGQPPRLIYHV FKRFSGVDPDRFSGSGAGDTFL E/ISGRVEA*DVGVYYCMQGT QFPCSFGQGT KLETKRTVAAPS
14549	44917	A	14635	3	652	AWWNSETPAQLLFLLLWLPHY TSGEIVLTQAPGTLSLSPGERAT LSCRASQTIGSTYLA WYQQRPG QAPRFLIYGASSRATGIPDSSSSS SSSSSSSSSSSSSSSSSSSSSQ YNNWPPGGTFGPGTKVEIKRT VGCTHLFFIPAHLMSQLKIWE LPSACVPVCNNFYPREVQYSYG KVDN/VPSNRVTPRESVTEQDAS KDSTLQPSAATLDA
14550	44918	A	14636	3	440	
14551	44919	A	14637	457	1270	SRRVSFPPSA*QAVSDPSRQQLP SLRLRWGPEGRSFP AENLGRGV RWVGGRDPLAA/LP*SSGPLNA GRLFARPQESGAPRIGNVRDVP RAREDVGTQAGREREFPRLFG PAAVVGCERHLSFPRAAGAG GRAGAAGRRSAPPGLGSCRSC RISAGPHGNDVPTLGGRGW/PL *NSGA EKL*EQ*G*/TGTSWSL AAILGGVPREP/IGFRGAGRETIG PRGWL/VMLSRVLLHSVLLCT CHSSWVLLHSDLACHADNNPD IQSCLFPMISKY
14552	44920	C	14638	90	465	
14553	44921	A	14639	116	439	
14554	44922	C	14640	278	364	

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14555	44923	A	14641	116	687	EIKDAALQLPLWRAQDRERAM KERREKRREREKERDREKKRK EKMFCRKRSCHTIMEPTPELSCV LPCLAPJVLAPPPLPLPVLP ATR*LPQQNRQSTL TEAHGLATR GPITLANRNCMPSTTRDRRLT PPSTLPNTTNLSWGVREGPNQD PEPSLSPCVPHDPFDYNAESLFS YWLVSVPMTAHTP
14556	44924	A	14642	474	1166	HPNRQGLRAPATAPGHPGREG ALCEAPQGPQKCGPPRAQEA Q/GTEPRRASRAAGACRHHWP QVAIRPGAGAPAGAARLGGV*E PGRAA/APRLPLPSQCCHR*GTS PAHLSASRSSSATCPWRRTAGR SGPSPCMTLAKQRQGHPRDGWI RAPSCDVTNRGLSSLNLGGSA QQLLLASRPLGSGSGALEALEH GKSRAPWEPWLHGTHNPVHGK DPAGSTSHWPRPPAPRT
14557	44925	A	14643	283	806	PRGSFSTGRTRNAAGSTSNCSL RSLSARIEERKVSRCVGVPNHR HLRLGALTTRTPSWNGAIPTLA KLPAKRC*RRSGRRSKTWSFPG ST*LGNF AEEMICAASARPAGV PGPALPTPLRAPLPGVPWTSSR GRMCARLSCC/HAGRPVPARPG AARARRAAAGERHRPPALRV
14558	44926	A	14644	1	338	
14559	44927	A	14645	1	1091	MSNDGRSRNRDRRYDEVPSDL PYQDITIRHTPLHDSERAVSA DPLPPPLPLQPPFGPDFYSSDT EEPAIAPDLKPVRRFVPDSWKN FFRGKKDDEWDPVSDIRYIS DGVESPPASPARPNHRSPLNS CKDPYGGSEGTFSRKEADAVF PRDPYGS�DRHTQTVRTYSEKV EEYNLRYSYMKS WAGLLRILG VVELLGAGVFACTYA IYHKDS EWYNI.FGYSQPYGMGGVGG GSMYGGYYYTGPKTFVLVVA GLAWITTHIILVLGMSMYRTIL LDSNWWPLTEFGINVALFILYM AAAIISM*MIPTRGGLCYPLF NTPVNA/GSAG*KEDR*LQ*SSC LSP**FISLVLWFA

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14560	44928	A	14646	398	1107	SPGLVCGLLIFCKVTVPICAGPY RCPFGGLRH*SAR*QPPSGLREN GARPPGGEWLCP*FPP*PLNSR WKLPPRLVT*GEPWAAGEKFP RLGAGTGPAAGEGLPRARDWE PGRAGPERWAPGRGPAGTPAK TAAVKRSAPLPGSGDYANGER KPPSPFCQVKSGLN*VLCG*RL SLPAA*KPKKA*RRGRRQSPGK TGYQVQQRPKNDPKSSIGPSP KNRQSLCLQPLWSFLIQ
14561	44929	A	14647	1	540	MGVRDPLEEAVCALAEQLQCA GRFAALFRASQERLSLLKLCPL QLPLPPRALSQGYKPLIGLLAF FQRCTAQRGGI*RGSLATVTLIS CGGLCPV*TSQRRCLPVRGKLP TQASVMANAPPRTLRQLHRSTS DCCAGSENFKPVLSLLGSVGV GSTELDHLAPWLQPAFQGEW FYLT
14562	44930	A	14648	169	487	EVCYYPSETYFCQFVKLILCPV LFPCWQGVVQPKLSCMRCLST LLRGVSQ*GYMGVRDPLEEAV CPLAELEHCAGRSALFRAGRQ ERLSLLKLRPQLPLSPSA
14563	44931	A	14649	1	210	
14564	44932	B	14650	1	1683	
14565	44933	A	14651	1	529	MDSEVQADDEVSDENGELIGN WGKGMGVSDDPLEEAVCPLEAE LERSAGRSALFRASQECLESL LKLTLTAAPSPRGTAFRSPFKS PAQRSSIIC*Q/LYSCKTFRSTVA PMPRLCLQASGKVQ*EN*SWA IPA*QGTSPMCSLCSGAPHQPG APLVLPPLPPVNRRLRELQCWL
14566	44934	C	14652	295	430	
14567	44935	A	14653	452	637	
14568	44936	A	14654	151	446	MVLSHWHSRCHWGMKKNYLQ LARCLPKWLPSFVFETQGPCDV STQGTLLVYGLQRPWEKHSI*A R*HHPSQHGPSQLPLARGSSP TPCASRMQRHPT
14569	44937	A	14655	2	335	EDRSAFRRPQPTHPLHPLHARS APKSPTPSPSPDTQLGLSGPTS GPESAPTA/PGNPSWRSSRWGSS SPCAASST*KSPYP*/CSPT/CAFP SPRLPFCRSAYQPAAGAGRGK
14570	44938	B	14656	373	502	

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14571	44939	A	14657	1	400	GSPAPAAAMDEERALYIVRAGE AGAIEVLRLDYSDKVKSPGPGR AVSHPRALRACTSHPSPPSPFR GCALPPPKTFPAWACVFVPPAF SIHAS/SHPTTPTVAPTPLIPGPA A*PPVLLSSVQVTPPESVDVHL
14572	44940	A	14658	659	1177	ARKGSALLRLYSNAWCVCVK VLRIFSTASAYITRRDSSLGPVW TFLNFSFGSPGEIPTPFFFFPVFP LPLVAWFCPASFCPLPQCPLVPS EPSPPPHSGDAHCSPPKTFPAW ACVFVPPAFSIHAS/SHPTTPTV APTPLIPGPA*PPVLLSSVQVTP PPESVDVHLCPVPHS
14573	44941	B	14659	1	318	
14574	44942	A	14660	2	131	
14575	44943	A	14661	354	762	CPEIRPPS*THGTHK/SHFPPTASG THSVLEAL/PDTRQSPSRVHQ DPSPAI/PALLSPHEHGQPHLL QLPSHRCHPDAPFNCDVAKAC PGHATAALEHPYLSGRQSPSP THLPKLPAGRGYTVCALPKPGG ERSAV
14576	44944	A	14662	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDAIPLL
14577	44945	A	14663	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL/DPAIPLLGIVPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
14578	44946	A	14664	1	1584	
14579	44947	A	14665	1	4729	
14580	44948	A	14666	1	1566	
14581	44949	A	14667	1	1424	
14582	44950	A	14668	1	576	
14583	44951	A	14669	1	3325	
14584	44952	A	14670	1	2195	
14585	44953	A	14671	1	3162	
14586	44954	B	14672	287	2018	
14587	44955	A	14673	1	1073	

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14588	44956	A	14674	1	3335	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTSHKASRRQE ITKIRAEKKEIETQ
14589	44957	A	14675	1	1838	MIIPIDAEKAFDKIQPPFMLKTL NKLGIHGMYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTTRQGPC LPPLLFNIVLEILARAIHQEKEIK GIQLGKEEVKLSLFADDMIYILE NPVSAQNLLKLISNFSKVSQYK INVQKSAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGKDSLF NKWCWENWLAICGKLKLPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNIELKSFC TAKETTISVNRQPTWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPIKKWAKDMNRHFSKEDIY AANRHMKKCSSLAIREMPIKT TMRYHLTPVRMAIIKSGNRC WRGCGEIGTLSHCWDCNLVQ PLWKAVWRFLKDLELEIPDPA ISLLG/TPYKDYKSCCYKDTCTQ STFTCRQHLPL

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14590	44958	A	14676	1	2354	MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFPSAPHRITYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRICKLTQNHSTTQQLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLKELEKQ EQTHSKTSRRQEITKIRAEKEI ETQKTLQKINECRSWFFFEKINKI DRPLARLIKKREKNQIDAIAKN DKGDIITDPTEIQTITIREYKHL YGNKLENLEEMDKFLDTYTLPL RLNQEEVESLNRPIGTGSEIAIIN SLPTKKSPGPDGFTAIFYQRYK EELRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTLTKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYQYN RDTDQWNRTEPSEIMLHIYNHL IFDKPDKNKQWGKDSL FNKWC WENWLAICRKLKLDPLIPYTK INSRWIKDLNVRPKTIKSLEEDL GNTIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWEKFFAIYSSDK GLISRRYNNELKQIYKKKTNSPIK KWTKDMNRHFSKEDIYAAKRH MKKCSSLAIREMCIQITTMRYH
14591	44959	A	14677	1	3144	
14592	44960	A	14678	1	2745	
14593	44961	A	14679	1	2742	
14594	44962	A	14680	1	3264	
14595	44963	A	14681	1	2982	
14596	44964	A	14682	1	3102	
14597	44965	A	14683	1	1443	
14598	44966	A	14684	1	3723	
14599	44967	A	14685	2	1841	
14600	44968	A	14686	572	744	DLLTTIRMPDVKKCSSLAIRE MQIKTTM*YHILTPVRMPIIKKS GNNRCWRGCGEI
14601	44969	A	14687	1	3588	
14602	44970	A	14688	1	5569	
14603	44971	A	14689	1	3992	

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14604	44972	A	14690	755	2415	QELRVSGWSPASAPANT*CP PAQPCPTRRSGGQAPARTSR PGSRPRTASALPRPAAQKA ASRSA RASRTNPYTAPKPL PSVESALQ EAAIGEHAQQR VSTCAAPA APPSPAWPWSA ARSAAPPRT*ASAPA*SPL /PVRLKSPGSSNC EARGEG WKT/PALPVQLGAHGPPQ PAAVPCASPGSGAGPRWS RSARRTPRGPLQGRGTWV SPDPGREATPSGTQWPQK TRGSLPGS*C APETPCSA A*SSGTSPPRGAGGC CP GTVPPALEGHN*PQRWGS HSGRVEVTRAEGPQCQQA PAGCSLGVGGQRGPPGLP PIPVPLC*TCRSS*MEA ATGSVEKCKRMA SLMQAS RWSFLRVAPVSGQVK Y TPGTARWAEPSLGSDDL VP GAS/RAPADGGFGLK FLSHLVS DGVLRCCGPR PGTASAPAGLR AAAA/ PSVPSLVGPWRGGLGAG WLGFSLWAFSPTDSLFS* PGPALLNLMSALNS*K NFFMVAARS CGGGTRGR GGTGPSRGRGRRR PATGR K*KKKKKKKKFTSPPEV PPSPGLPRDNL
14605	44973	B	14691	1	822	
14606	44974	A	14692	1	2789	MAAVRKQLPRGVLGYGG SGLSTAAADTSLLLGSLQ ERKSAS AGPGYLRSVA AWSGLWLTGA SEAHSV VLACFSRKDVEASLSV GLPVHPDASCARRLDA ADGVA GGSPLPQSTDG WRLTAHSLPQSTDGWRL TAHSLPQSTDGWRLTAH SLPPP TDGWRLTTHSLP QSTDGWRLTAHSLPQST DGWRLTTHSLPQSTD AWRLTAHSLPQPM DGWSCRSQWCV
14607	44975	A	14693	176	440	
14608	44976	A	14694	114	253	

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14609	44977	A	14695	124	890	GSRAWDRPRLVAAATTTLFY GYGFVSAELKKASKRMTCHKR YKIQK\KAPEHHRKIRGEAKKR GHNKPRKDPGVPNSAPFKEAL LUREAELRKQRLEELKQQQKLD RQKELEKKRKLET*SWIFKPSN VDPMEKVEFGLCKTENKAIRSG KQNSKKLYCQELKKVIEASDV VLEVLDARDPLGCRCPQVEEA VQSGQKKLVLYLNKSDLVP KEDL\ESWLKLF*RKDLPSNGCF RASTKTQRVKGKITKVSFIS
14610	44978	A	14696	553	997	EVTACWSSQPSLTLGASSAW APTLAALIEPFSPLLHCGSPFLG WPRLEPAPSAPPWAPVRPEPPQ QGPPSAPGRPISTTQGLRSADA GRRTGTQLHRQPAKVCFS/IS*S QRDHEPTRRNEQLQTRRLKSCN THREDLQLHSRRKKL
14611	44979	A	14697	1410	2036	
14612	44980	A	14698	3	630	RYKGSRPHQTQEPSWLHLVDP APGLQVELPASPAPCARIQPL GGRWDWAPWSRGWCSSGRLG QHRSPWSGWEAQAWRAAGPK PCPAGRQLRPGKSSTAPVGRH CWGIQYTLRSHWPGC*VPHSSG PAGLAGCSGTPAGPQAPHAAP VPARA/CSLHTSLQAEGVGSSL GQPRKGLPQCRWGLKGSSNAA KVGAQAGEVQARALRTAS
14613	44981	A	14699	190	383	ASHPLRGLRSGRSLPDERHRL HSAQSHRPPKG*GVRAGAGL T/WQLHL*PQCGIHWWKPAAGLL
14614	44982	A	14700	1	1095	
14615	44983	A	14701	1	777	
14616	44984	A	14702	1	933	
14617	44985	B	14703	1	996	
14618	44986	A	14704	978	1207	ASLPLRGLLCCPSLPEERRPLLH GAQSHRPPKG*GVRAGAGLA/ WQLHLRPRCGIHWWKPAAGLLS LGPHQQSSKSA
14619	44987	A	14705	111	558	

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14620	44988	A	14706	1	1103	MKPWALKVSVTALKVARLEFV PPDVRMCSEFLPCGVKLQTFAY SVTALKAAARLELFVSPGGLVVS LASGVKLQTFPVSVTAHKSSVD PRSEQQDLLQRAKEQTFHTVE GDRSGSPDSSGAQLASPSGSR RAAGGAACQSRALRPHSSALG WSMGLGAVEQGAVALIREARAA HEPMERVGGSGMAGCRSRALP REKAAKARRETEGSAAVSGWL SGIAQWPKIDHEGFRAVKMPQ AAWLLKAVTFIDLTTLSGDDTS SNIQRLCYKAKYPIREDLLKAL NMHDKVAAGFPAGQTHLKTRL EEIRLAVEDGATEIDVVINRSLV LTGQWEG/LYSPVVYSALPCNI* HSRLFLPSGNALLWLWCLHS
14621	44989	A	14707	2	2300	
14622	44990	A	14708	2	1058	ARSNIRMVTAFRSLPAGSSGAA RA\MSAHNRGTELDLSWISKIQ VNHPAVL\RRAEQIQAARTVVK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGITTAAVCVYP ARVCD\AVKGTSPAG/CVNIPV GISRAAGFPAGQTHLKTRLEE IRLAVEDGSLQKIDV\VINRSLG A*QAQWEALYDEIRQFRKAC GEA\HLKTILA\TGELGTLTNVY KASMIAMMAGSDFIKTSTGKE TVNATFPVAIVMLRAIRDFFWK TGNKIGFIPAGGIRSAKDSLAW LSLVKEELGDEW/LKPELFRIGA STLLSDIERQIYHHVTGRYAAY HDLPMs
14623	44991	A	14709	576	998	VLQFLKAACPEFVPSGVPMCE YLPsGGFVSLASGVKLQTFPV SVTALNALRLELFVPPGGLMVS LASG/GSCRSSR*VLQLIKAVWT QRPLGGRWDWAPWSRGRRSFG EARAAQKPMEGVGGSGMAGC RSRSPAPREGS
14624	44992	A	14710	2	589	RHHPRHVAQARFPFAPGLAGA QRGSGAE*RGPGGS/PGPAGLS GGESL/PGETDRGADKEERGRQ RWQRALGRLSAGADPLPAELR GRRQRGR*AGQRAAQEAACE APIQSGARGNRG*GRRL*GC YQ*V*FPGLTRGWGRSRPSAV HCGWEPP*AGKPSGQTPRHSG* PAGVVDGLPPKVTGPPPGTPQPR

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14625	44993	A	14711	1	1596	MRLTRCQAALAAAITLNLVLF YVSWLQHQPNSRARGPRRAS AAGPRVSLPPHPLTCVWRCSR AMDRPPAASRPETTVAIEFVAL VLDGARAEAHALLERMVEALR AVSARLVAAVPVATANPARCLA LNVSLREWTRYGAAPAPRC DALDGDVAVLLRARDLNL PLARPVGTSFLQTLRGWAV QLDLTFAAARQPPLATAHAR WKAEREGRARRSALLRALGIRI VSWEGGRLEWFACNKKNQRC
14626	44994	A	14712	225	980	VPSRTWAEYRTRFVPHSLGQPR SSHIPQSPQTDQTAQQQALAP PAGRSGQ*GRPGRRLGPGER HS*APPPLSQLLQTFPHLQALP SAHARPSGQPHADRHSRSPSG /DLSTSSVLKVVVPQAGGPKQA RCPQAGRVCHCPRGGRRGPE/Q Q/GG*RPEAPQASPEKGSTGLRP SAKDSKNQGTGIFLRQCVAPRP EALCCPPPRGADTPVSPCLWVA GAGIPLQPPEGAEGAVLGSCLT LCPGSPDSPPTS
14627	44995	B	14713	405	893	
14628	44996	A	14714	178	499	
14629	44997	A	14715	231	436	
14630	44998	A	14716	141	393	
14631	44999	C	14717	97	351	
14632	45000	A	14718	119	358	
14633	45001	A	14719	21	614	PPCTSLRPLHAFSGKMTLNRG TLSLDSQLHNLIALQMTCFKD VEIPNFFWEPSTPSHRNIMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGGGYLSSDVSSSP RKAASVASMYTVITSMNLNFIY SLRNRDIKGVL RQPHGSTVQFQ YLLICSIPIFVVVWVKKGSKVK
14634	45002	B	14720	162	1263	

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14635	45003	A	14721	696	1791	VWIALKSENITCELLLFKMQTQ CQVLVYLFPFQPSFLGKRCPIS TDPQNLTDVSIFLLLEVSGDPEL QPSPCWA VPCCAWVTVLGNL LIILAISPDSHLHTPMYFFLSNLS LA/DIGFTSTTVPK/MIVDI/QSHS RVISYAGCLTQMSLFAIFGGM E/DMLLSVMAYDWFVAICHPL YHSAIMNLCVGFVLVLSFFFFA LSLSDSQLHNLIALQMTCKDV EIPNFFWEPSQLSHLACCDFTN NIIMYFPTAIFGLPISGTLFSYY KIVSSILRVSSGGKYKAFSTCG SHLSVVC*FYGRGVGGYLSDD VSSSPRKGAVASVMYTVVTPM LNPFYISLRNRDIKSVLRPTEH CLISKK
14636	45004	A	14722	1	1971	MTRKVTLLLRRTWRGGCGRLA MGMEATPQGS LHPLFQEHWIR AEDFGLSPMHPNSVQGVDDM IRLGDLEAGMVHNLIRYQQ HKIYVSLSPVSTGEPLTGANLL DREKMMHHRGHCPIALTEGVS GPDNPEGRARAKAKAKARAE PLPGAEGTDHLLPSQTYTGILV AVNPFQVLPLYTLEQVQLYYSR HMGELPPHVFAIANNCYFSMK RNKRQDQCCIHSPQNRVGAQTDT VLKVFQHLLISLICKTTLQACCI PSHPYLSAPGPPPLTTQCRSYS DSLGPQLFGDVVCYNCSHVIEG DGEALCSLPHTCSGAWVLQL VSPLNKA WCVSCFSCSTCNSKL TLKNKFVEFDMKPVCKRCYEK FPLELKKRLKKLSELTSRKAQP KATDLNSAEGPLAQLGAVGA/V TGITHEPHIPQVENGSQLDDV PALGVENWRIFMAERMEAQ GQRLLLSTMHEEYEFVSPSSVAI AELVALFLEGLKERSIFAMALQ DRKATEGGPVGLTKKQGLLAS ENWTLGQNDRTGKTGLVPWH CLYTIHTVTKHSDSCCTA VPTL LEASSGCIFMSYKKHITLTPKSA DSNKRPS TLGSQFKQSLDQLMK ILTNCQPYFIRCIPNEYKKPLG FSDSFMLIKLIRIDK VQYDSFSYI

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14637	45005	A	14723	1	1197	MNMNKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSRKTLMTHQSTCPKH RASRVGPSNLSQNKQTVKKGD QTSVRRKRNDLKVEERHKNNH LARELTSSAAAAAPTGHAAATA QAPQRHVEVGRAAAPAGDLGE GIVGEQVLGAERLVGPASRAR ALCVLGDREAGHTAEMTAAP PAQVPGPGGPTALRRPSSYLGL GVDEQNPMSSVDGEDDVRVQ HQELRDCLIKHTILIRGEFVTRS LNIAQAADRRDAFVKGIYGALF LWIVKKINAIFTPPAQDPKNV RRAI/GLLDIFGFENFENRIIRT LCWRYREARC
14638	45006	C	14724	1	1032	
14639	45007	A	14725	1	4960	MSTTSIFQQLNLLSHSHKQKQ QIQLPNGRSRYSLMAAFRMQ YFLSLPMKSLILVGFERLQAIAR SQPLARQYQAMRQRTVQLQAL CRGYLVRQQVQAKRRRAVVVIQ AHGQGMARRNFQQRKANAP LVIPAEGQKSQGALPAKKRRSI YDVTVDTEMVEKVFGFLPAMI GGQEGQASPHFEDLESKTQKLL EVDLDTPVMAEPEEDVDGLA EYTFPKFAVTFYQKSASHTHIR RPLRYPLLYHEDDTCCLAA
14640	45008	A	14726	86	370	RTWMTHVWRRRRVQAAPTAY SSFRPGTSPCPAQPRAGARA*TR SGTSIMPTGFSSHTSCLTVPAFFT ASSAGQHRQRHRKTTAAGHPT TTGAASF
14641	45009	A	14727	3	455	MQSVLPAAHVSSSTRASSRVTL SSPSTSTNCRGRKSSRVTLSPVG SGPGGGGGGPGSGRFGIDPPRK FAAAGSFSTGAPSSVMVVRVSG MPSLSW*QYP*SCSTLGCRRSS STISLSSLWA/VQPIAAPPYELA TQLPISCR*SPSPCAPS

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14642	45010	A	14728	338	1782	NQLSK*KAHSIRT* TALQSSGR SQICIVQSSADALPSSRCTNPSSST FTPTPLPPRPHPRCTSTLGCRRSR SSSTISLSSLWAASR*QPLRTPN SRTQLPRSWPLKSTALSPPPPGQ ATRLCWWMVSSK*RTWMTHV WRRRRVQAAPTAYSSFRPGTSP CPAQPRAGARA*TRSGTSIMPT GFSSHTSCLTVPRLHCVCWTA SSTPQESSPGGWTRPWPSWRRRC CTCTGAGRYLQNSTAS/T/VPVS TSVSQTAPSPKEDYRCWPSYHH GSLPPFSVQPG*GCGMSVRAMP SVGPLWSPTPPGQIKRQNYLL NYWSCWKMTLLAGIIPSS/TS RPADLDYFLGSSQCPRDERTLK GHVSCDPTSSISITGEKLKQKLE S/SSTLADTKSAFLQDSWT/SSLP TLGASAIURTSAS*TDQCPPAP GPLHVSE/SLNSTYPSRLCSSTCS TVDSFQIIMPN*MPFSTCGAFC WCLWFSAITALYFVM
14643	45011	A	14729	148	1040	WCTGSGFSKGTWEILLRKKPSL GNVGALPCVATACLTTVEKRA PRGHPLAPVLGDIKPCVGSMS STSEL/CTWGNFEFWGRNKYNH WF*WGWALLHQFKMGKGAQG LQEAIFYRKDTY*A/TMP*NPIG ISEFGTLALPGCKNVFERFMS RFELPGKAAAMTDNTNVNYVR YKGDYYLCTETNFMNKVDIET LEKTEKMWKPRFRGICPOLQG CSVTEQGFESDDAKSWALQH PKRPAQQDWAMSRGNQGWAN LGLKIIRGEAVTTAKEVSVVL KVLEVTDGKVVAREKKLRDSR
14644	45012	A	14730	189	507	AAGADTSQGGGGPPPSQSR PKSPSAGRKGSQLSPOQPQKGL PSPQGRKSPASSKATPQASEPV TTQLLGQPPQTQEEGSKAQGM PPQRLGASTQQQTNQEAA
14645	45013	A	14731	2	356	DGVSLSCHPGWSAVALRSQLTAT SASWAVCWQGCGETGILLPCW WECEKVQPLWKQYGRSLCEDH LNS*VQVILTTQPILFPKWLHL FTFPPTGQKDSSTFTLPTHCPG GRGCELSRHRCTPAWVTE

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14646	45014	A	14732	1	408	FFFFFYTTFFLFFYFYFFEMESH SVTQAGVQWYNLSSLPQPPPRF RRFCLSLSPSS*DYRCPPPHPAN FLCF**RQGFLLAKMVSIS*PH DPPTSASQSAGHVLTSKWELNI EYTWVIKMGTDATGEHKNKEG WE
14647	45015	C	14733	262	536	
14648	45016	A	14734	179	745	TDCLHNRCHRSPRSPPPGPPG*R SRADWRRGRGWGSWCASSR RVC*RCAPASAFSCCRSPRGRQ GRTFPPSPCAPD*TQ/PVSPGDS TRPCPPSPSPAHRAT/GCCGRR RLPGNASYLA SPGKEAGEFPAS QGDS*PGQYGYIGDSSS/RPTRG TWMKASTPRHPIAPQICGA*G FGEHQEVVPREK
14649	45017	B	14735	1	1164	
14650	45018	A	14736	35	542	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGAL PLDVTFTFY/KDYDGKLNMLSE KYKLDKESYPVFYLFDRDGFEN PVPYTGAVKVGAIQRLWKQGG VYLGMPGCLPVYDALPGEFIR ASGVEARQALLKQGQDN
14651	45019	A	14737	11	908	VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSG/LHTKGA LPLDVTFTFYKVIPKSKFVLVKF DTQYPYGEKQDEFKRLAENSA SSDDLLVAEVGISDYGDKLNLM NELSEKYKLDKESYPVFYLF EGDF/EEPSHYTGGS*RLGAIQ RWLKGKGVYLDGDLVCT V*LTPWSGFIRA/SGVKARQAL LKQGQDNLSSVKETQKKWAEQ YLIKMGKILDQGEDFPAEMTR IARLIEKNKMSDGKKEELQKSL NILTAFQKKGA/EKEEL
14652	45020	A	14738	3	227	
14653	45021	A	14739	1	424	
14654	45022	A	14740	1	207	
14655	45023	A	14741	2	352	
14656	45024	A	14742	1	441	

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14657	45025	A	14743	1	461	MTVDYRKFNQVVTPTMAA/AVP DAVSLLLEQINTFPGTWYAAIDL ANAFSPVPVHEAHQKQFAFLPQ GYINFPALCHNLIRRELDFFLL QDITLVHYIDDILLIGSSEQEVV NTDLLIHKRSKEAEHTAASRIR VSCLPEQKSHEQTLTPWEQVP
14658	45026	A	14744	1	928	
14659	45027	A	14745	283	1074	
14660	45028	A	14746	450	1970	VRVLSVPVEKELKLWKNTHKLL SYPTVGAAVTQLQNLAMGVI GSHGARGQVVALNRQRQGD QPFTRTVHVWGKGYDRFTWGL LDTGSELTLPDGPKHHCPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHTSLTGIMVGKAKWKQ LELPLPRKIVNQKPYCIPGGTVE ISATIKDLKDAGVVIITSLFNS PIWPVQKTDGSRMTVGYRRL NQVVTPTTAAAPDV/VVSLLE QINTSPGTWYAAIDLANAFSIP VHKPHQKQFAFSWQQQYAF VLPQGYINNPALCHNLIRNLD HFPLLDITLVHYLNDIVLIGSA IKWVMHSS/DSIIKWKWHVHDR AQADPEGTS*PGYGHFWCPIC QQQRPTLSSQYDTIPWAISQLPG DRLIIGPLPLWKGGKFVFTGIDT YSGYGFAYPACNASAKTTIMES QNTLSTLMVFHTALPLTKALTS WLKKCSSGLMLMEFTGLTMFSI

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14661	45029	A	14747	1	2589	MGPPYKPPTTWPPQTLTSHSTT PVKLQSLSLPPTAARGATEPCH LQAPASSVQOMTPPAPGLKHL GGKSQMCLEQDGRSGSVRGSP CHAGHWVAGAGFGKGTTRTW GHVNLIVPPNCPTASSAARDS APNQPLLGVVTAQIVPPTCPA MTVQELIAPLTLPPAAGCRRGV RPFQTRVWLLAQLLRARLGGP GEGVVTCHSWRLERVAPRLAS LWWALAAETAARLDWAACKRP SAWGSIKAAEFSSKATPRLEGA SSRTLWVSYIAKETTTGKNGP VEPSHLWEAYCRATAPHPA VH SPSAEVTYTCGIVNLLQLGLVP KSHLEHTGCHVVVELIICSVV LPLISRLSDPDWIHLVLMVIFSK ARDPTPCASGPEQPSVPTSLPL IAEVQQLPEGRAPSPVAAPGFLS KQIQDALCALEGSQALEPKGGE GSEGVAEAGPGTETETVLPVST LNFCEPIQIDIAKIEIEQGEVTT VTALLLEGLEKTCSSRPSCLEKD LTNDVTYLDPTIFSEPLSSPDG PVVIQNLHITGTITAQELSGTGL QPCTRYTVKCETSLDGENSSLQ QLAYHTVNHRVWEFLNLQ/SH QEKKPDL*KFKINIEKMVVSAL VDNLKTAFCSESQGPTEELSE AETESKSQTEGKKARKSRLRFS SSKISPALS VTEAQDTILYCLQE GNVESKTLSSMGMESFIEKQTK
14662	45030	A	14748	478	3507	SKILRAVIWGSHLVRSAMKTET VPPFQETPAGSSCHLNNLLSSR KLMAVGVLLGWLLVIHLLVNV WLLCLLSALLVVLGGWLGSSL AGVASGRLLHLERFIPLATCPPP EAERQLEREINRTIQMIJDFVL SWYRSVSQEPAFEEEMEAAMK GLVQELRRRRMSVMDSHAVAQS VLTLCGCHLQSYIAKEATAAGK NGPVPSHLWEAYCRATAPHP AVHSPSAEVTYTRGVVNLQ GLVPKPHLETRTGRHV
14663	45031	A	14749	1	417	
14664	45032	A	14750	34	350	RERGQEGGVAGRVEMDVSVVE RGAYADQIWGRPKGGESRGEK RKGRWVQRVRLARVTPAGL GECKWGRGRGD*VRRVKPRAL REKWDGSTVSDSTPMKPGLE

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14665	45033	A	14751	1	1604	MASKRCIRDFRSRGGKLSFQL YATFRKEGCGPVLANGNPGGG RGQEVSA TQDLRRGWGIASSAS RFPWRQSWPGRPRLGNYDSGA PGEAKMPKSGKDKKKGKSKGK DTKKLIKTDSEVVDRAKANASL WEARLEVTELSRIKYRDTSRIL AKSNEDLKKKQCKMEKDIMS LSYLKKQDQEKDNMIEKIKQQ LNETKEKAQEEKDKLEQKYTR QINELEGGFHQKAKEIGMIHTE LKAVRQFQKRKIQVERELDDEI NDLLVKEKIMQLVQQRSQIQT QKKVVNLETALSYMTKEFESE VLKLQQHAMIENQAGQVEIDK LQHLLQMKDREMNRVKKLAK NILDERTEVERFFLDALHQVKQ QILSRKHYKQIAQA AFNLKMR EHVQEEQNIPKSEHLMAESTAP V*IRIFWRPKNGHILKEMWILEI *PGSRKKYCDCLQK*MAVLL GNTTQSSRPSSSRMTLFLDSGET KEFGDESKLDKIFITQQAISD VFW*SGATHYSKRTSGV*HSGK SESLOPRGQRLI
14666	45034	A	14752	95	473	
14667	45035	A	14753	168	449	

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14668	45036	A	14754	1	2000	MAFEQAKQVVKLALDLWPIGD GPVELQVTVLDQHANWSLRQE QHKGKRGPLQFTDVAIEFSLLEW HCLDTAQRNLYRNVMLENYRH LVFLGIVLSKPELITCLEQGKKP LTVKRHEMIKPPGQKNWEKQ ALPLTGCLTKYPSWAKNIDHVT CSHFARDLWPEQSIKDSFQKVT LRRYENYGHDLQFKKGCEV DECKVHKRGYNGLNQYLTTTQ SKIFQCDKYVKVIHKFNSNRH KIRHTGKKPFKCECGKAFNQS STLTHKKIHTGEKPFKCECG KAFNWSSHLTTHKRIHTGEKRY KCEDCGKAFSRFSYLAHKIIHS GEKPYKCEECGKAFKRSSNLTT HKIHTGEKPYKCEECGKAFKR SSILTAHKIIHSGEKPYKCEECG KAFKHPSVLTHKRIHTGEKPY KCEECGRAFKYFSSLTTHKIIHS GEKPYKCEECGKAFNWSSHLT THKRIHTGEKPYKCEECG/KGF KYSSSLTTHKIIHTGQQPFKCEE CGKAFKCFSLTTHKRIHTGEKP YKCEECGKAFNWSSSLTAHKRI HTGEKPYKCERCCKAFKRSFIL TRHKRIHTGEKPYKCEECGKGF KCPSTLTTHKTLIEIHAGKKPNK *E/ECCKAFKDTALTRHKIIRTG EKPCEFDECRKAFNQLSTFTKY
14669	45037	B	14755	269	1131	
14670	45038	A	14756	2	149	ALFRAGRQECLSLKLCPPQPL SPTCFVPGR*GFYLHFFQRCAA QRGGI
14671	45039	A	14757	2	175	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
14672	45040	A	14758	1523	2667	PLLVIHRQTGSGEDIQQTPADL QQRDLERKLTNRNE*HQHQQ KRHPLKNPTQMSP/CIKDQRYIN PRSTIKLELGIKKLTENCCTTTWK LNNLLNDCWEKQERSKTDLT TSQLKELEKPEKTSKASRRQEI TKIRAEKKEIGTRKTLQKINKCG SWFFEKINKIDRSARLAKKKRE KNQIDTIKNDEADITTDPMEIQT TNREYKHYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TSSEIEAVINSLPT/KKRSPPGSDR FTAEFYQRYKEELVPFLLKLFQ TIEKEGLLPNSFYEDSILIPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHNNQIDFIP GMQGWFNHKSINVIHRLNR
14673	45041	A	14759	640	1771	APVARMATA/PLFYTALLVFSAL GNILALCLTCQ/KRRKINCTGIY LVHLAVSDLLFTVALPGRVVC YVLGSSWPFKGKGLCRLTAFVL YTDYGGVYLMACVSVVDHYPT VVCAHWGPCLRTAGRARLVC VAIWTLVLLQTMPLLLMPMTK PLVGKLACMEYSSMESVLGLPL MVLVAFAIGFCGPVGIILSCYM KITWKLCASTAGRTQ*PAGKDTT GGASPPGSPDQPEKTPPAGAAQ EDPVTPTRETPPAGQPERTQ*PA GKDATGGTAREDPVTSRKGRH WRGCLLTLLMLVAVVVCFSY HLNIKQFMARGMLHLPSCAER RAFLSLQATVALMNMNCGI/D PIHYFFASTHYRKWLLGILKLKG SSSSSSSSSTLY
14674	45042	A	14760	1	401	MVLVQWLTAITSAFWETQNK SLQFEDK WDFMRPIVLKLLRQE SVTKQQWFDLFLSGATLQDSSG PLLTGKLKKRRKVSGETKY/IEAS SATSLKATTDTHLLLYNPFWI PLTLI*HLCWLQRF*SCDTPDP P
14675	45043	A	14761	184	2720	
14676	45044	A	14762	34	251	
14677	45045	A	14763	2	452	LQIEII*ALEELAAKEKANEDAV PVCLAADFSPAGMGSSCDGQE DELDIKSRAAYNVTLL/NFMDP PKIPHLKEKPYFGMRKMAVRW HHAENLVDRPQEESEDDSHLE GRDLDTWHVGVKISWDVKTTPG LATPQGDYCFMLGNLWRTKIL

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14678	45046	A	14764	1	1701	MPFKCKKQHTFNKTSPEGAII FTHGCLCTSPFNSELSHGLNL KLSSWEHLHRRSQQTLSVRLH VPTQPVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPLWQL KYPKLILREASSVSEELHKEVQ EAFLLTHKHGCLFRDLVRIQGG DLLTPVSRILGNPGCTYKYLNT QLFTGPFVPKGSNIKHTA*IA AVCETFLKLNLDYLIQETIQAEE LAAKEKANEDAVPLCMSADFP RVGMGSSYNGQDEVDIKSRAA YNVTLNLFMDPQKMPYLKEEP YFGMGKMAVSWHHDENLVD RIQLQLWDPVDGTTASSAVPKQ GRDKRREVPNTLSQPNSEQGLI SAFHSRCVHAVFYKLTSAPKTT SLPDVPSDLLAEGLAASRAGQA LWRCDDKSLTLVRKJNLQKG RDGGRSATNQSQPHLDNTGL ERQLEQKVGRCSRSPWRGLGHL EGNAQKGHLLHGVNKNQGHL LRRHGV SIRAGRAPHLAAADT APGRISCLGHSEALKPRIQAGGL GAESIWWQLWEGGSNSSVFGR HDEEPAALPLPGKQASGGHMH
14679	45047	B	14765	16	1462	
14680	45048	A	14766	89	566	MEQGSIIQAWREDALVLTQK GLVSKISSPKRPHVCHILKAPFC CSCTQHVGQSSSPR*ANPHIRRE STPIAMSDQLQRLQYQFYQIPG TCLLPEVTEKNQGRICMVTDL ETLVHSSFKPISNADCLVPVELE GTMHQIHVLMRPMYDEFLT*M EEMF
14681	45049	A	14767	1	305	LSGLEMFQAGAGAPSSPGY*GS CWAISWSGPPDKHSNRGASCG LETWAGAAATDTAGHPHAAAGR C*A*AGSGGQGTGSTAPLPAT P*PLQSLV*AAALPA

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14682	45050	A	14768	1070	2653	SLKPCMACL*HS*EKTLSDDSG RSWICAVSPGSPGPAAPLPEL SFPLRPGYTKLLPHATEEVSFPG SGAGRKLGPMLPSTAELCPGTR ARWSEGYRDLGRQAQDLQAG RKS VVTWALEGHPREERAAA KVQQCQRMWEGCSDPQELIPR PGRNPDVPDSAVALLPWGPSR VPDLGPDSEHR/PAHSRVQYWL HKAPAPSPSPQLAEPATPPTRP SSPGSRSPSSWHRLRSWSLNAD PWARPRADLPPGNPAPPSRGGA HGTWGGKDVRLGRGSRFSV CGRREVQRAARRV GTTGPWGR APGREERAASR*QPPGTG/PASP MGRASSSGSRVSPGPIRRTAPW EGCSCRSRHHWGKGLGPPDGE PG/PGSS*VAQPTVGGRRSLGPG GAAPARDAAAATPPGDAAARE GSGRHLRAPASRPQHQPSPRS HPPASATTASLQKFRSASSEPPS EDRPFDFSPATPPQCPRVAPSAG AR*R/AGGRLPE/PR/RPGPWGG GSRTNLTIPSTLHGPTAAARTS PHRKS
14683	45051	A	14769	748	1073	SQHFGPRWVDRLRSGVRDQP GQHDKTFSLLEMQKIAGRAGG CL*SQLLRRLRQENPLNPGGGG CSELRGLCTSVWATGRDSI*K KKKKKKKKRPWSLLSLIVLVQF
14684	45052	B	14770	59	466	
14685	45053	A	14771	2	3184	HRTGIPGSTISSPGGETVPE/MTA AMRERFDRFLHEKNCMSDLA KLEAKTG VNRSFIAL/GVIGLVA LVLVVGYGASLPLQLLGFY PAIYISIKAI/SPNKEDDTQW/ V*TYWV VYGVFSIAE/FFSDIF LSW/FPF*LHG*KCGFLVGWCN GPEAPSKWGLKLL*QAASSGPF LSLEATKSQIGQVLVKDALKDQ GPKETADAIH*KPKKSLP*ILL G*KKKK
14686	45054	A	14772	14	455	PQFPCRRFRALSEEELDNEDYY SLLNVRREASSEELKAAYRRLC MLYHPDKHRVPELKSQAERLF NLVHQAYEIVVERRTPAEIRE EFERLQREEREERLQQRTPNPKG TISVGVDATDLFDREYDEEDV SGSSFPQIEINKMHISQ
14687	45055	A	14773	328	479	

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14688	45056	A	14774	15	1095	KVAKMATALEEELDNEDYYS LLNVRREASSEELKAA YRRLC MLYHPDKHRDPELKSQAERLF NLVHQAYEVLSDPQTRAIYDIY GKRGLEMEGWEVVERRRTPA\ EIREEFERLLREREERRLQQR TN PKGTISVGVDATDLFDYDEEY EDVSGSSFPQIEINKMHISQSIEA PLTATDTAILSGSLSTQNGNGG GSINFALRRVTSAGWGGELEFG AGDLQGPLFGLKLFRLNLT PRCF VTTNCALQFSSRGIRPGLTTVL ARNLDKNTVGYLQWHCSSPLL QVQRPHRNTRACAPESFRPFL HVPTWDAECSGARTPSTAWTS AAVKLREACLSGPGSGSHQLLL LTPRSKRRTGGG
14689	45057	B	14775	508	1765	
14690	45058	A	14776	2	639	GRRRHRRRRHDCSRGDCYLPT GTNTQQPLPPPREPLPEL PARTP DLSMQNSEGGADSPASVALRPS AAAPPVPASQORVLVQAASSNP KGAQMQPISLPRVQQVPQQVQ PVQHVYP AQVQYVEGGDAVY TNGAIRTA YTYNPEPQMYAPSS TASYFEAPGGAQVTVAAS/SPF AVPFHSMVGITMDVGGSPIVFS AGAYLIHGGMDRPELLANL

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14691	45059	A	14777	1	2091	MKPPDDNSTQNEGGQSFEEERHETLQVRVKFRGGPKTAPGRKLIATLGQMNSGTSGGQVRVPGEEELMAGGATCLPNTAEHQPIRMKNLHTPAFRLCPLTLQDNEADAFWHQAFVDWGMPTGKKPQTLGLTYKTTHDLSMQNS/EGGADSPASVALRPSAA/APPVPASPQMLPLELVILGVV/PLDKCIPAQWSKEGQTNSYTYNPEPQMYAPSS/ASYFEAPGGAQ/MVGITMDV/GGSPIVSSAGAYLIHGG/MDSTRHSLAHTSRSSPARSFRNSKAPSSRKFCCLPTLSSKTL/SLFSKNLLRKLPLGKIISPDSVQWPWYIGLLVAGSESLASLLFPKASSSGETLGFATGQLAGESRLPSLLAFILVPIDVAVGKEQLVTQTTVYRVQSGQHNLKAWQEPALVNICGMGEKVDVQVGLCQHRAHLDGWNSSRAASVWPGETLTHHQDQCQANLPPGIETSLGKRGARYPSQEQGGGRVWLERLDPRG/AVSGTDL*CLPQSDVPPGRA*SGGTGDKSISTHDKSGRGNISKYHY/YGIRLKPDSPLNRLQED/TQYMAMRQQPMHQKPRWCRAELGGAGSPLGMEDEVSHVFPFPA PD/LGSFLLQDGVTLHDVKAL/QLVYRRHC/EDVV/MNLQFHYIEKLWLSFWN/SKASSSDGPTSLPASDEDPEGA VLP/KDKLISLCQCDPILRW
14692	45060	A	14778	94	3006	RTRSLTRKAMAEHAPRRCCGLGWFSTQQVKVVA VDAELNVFYEESVHFDRDLPEFGHVLVDVHGVHVKDGLTVTSPVLMWVQALDIILEKMKASGFESQVLALSGAGQQHGSYIWKAGAAQQA L TSLSPDLRLHQLQDCFSISDCPVWMDSSTTAQCRQLEAAVGAQA LSCLTGSRAYEFNLVCDRKHLKDTTQSVFMAGLLVGTLMFGPLCDRIGRKATILAQLLLTLIGLA TAFVPSFELYMALRFA/GL

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14693	45061	A	14779	1	710	MGPAAGAPTSRASRGPRAPALR AAVGRRCPRPEMPCQCHPLAR CGLDPAWTQLPQETAGAPRQD PRCTNQLICEHLPLEGLGFVYL GNKDSLRLHVKVVAVDALNVF YEESVHFRDLPEFGGLASSAV TQSSS/DDLQQVP*SLQSLHAA* SLQTNASPFTFEHSFLGKRHPK GAGQKRAESPTRPPLRLQEAAAP GELQRPLPYGTQVPAGLCPSVS GLRLRARALLPYRTHLSLV
14694	45062	B	14780	1	252	
14695	45063	A	14781	73	198	
14696	45064	A	14782	762	1080	AGRAEMQQRRESHEEAKDPSP LSPREGSQKQQNVNTSTPSHC PR/PPLRMPPPAPRRPV/CDHPR AECEKRAQHWQAAPAAPVR DPLGEASWAPESGGDVESLYI
14697	45065	A	14783	1	309	MTKTEREQNEQLDGGGYGERL GEYSLFLLCVPELNLQNGKICERV SSYFGMNLGGVLLKLPFPPTRE SWPPPHFTGTPHNHHGGVNSNG ALGCAQRCSLHHATNAGGWER GGVNSNRLFFLLSASFSDAKIK PAPSPIDHLRAEEC*/PPPLSQPP ALVAWCREHLWAHPKAPLLTP
14698	45066	B	14784	1	471	
14699	45067	B	14785	1	1143	
14700	45068	A	14786	1992	2205	WRSMGLRKRQLASQISYCP WS/CP*EESHCRRVSPAPLA*LL SPCPAPQQRSHDTPPPFFKHFP LPFSG
14701	45069	B	14787	389	973	
14702	45070	A	14788	287	525	TNPFNLLQH*KKP*CYTYISITD PTDACHKNKAFSSPAVSQLT/CI FSSTAGSFFVLGSHSCGHVAFS LWPRSPQLPGTR
14703	45071	A	14789	475	616	
14704	45072	A	14790	1	704	MTKWKSNPQHIMELQRTLSNP NNLEKSNVKTYYKAKIFDDNLI QLTFQQHRQDRDTEQEKKEE EREKRKQQQEPLRKKAKMQTV RPGFDLTQGPNCILTPHGKTWSR LPPKNHRRPYSRPEGPRVKA* NHGPEGRRGTRLPPAAKRAQ AEEAAQ*WPTSTRLRELVTPRA MPPSPSEDPVAVGHPAPPRGP RSDS/APLRPQLRPRLSLASE PAAAGNARGHRSVLALY

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14705	45073	A	14791	200	408	SPHLMSINLITFANFLFPCERNS QFLKS/SIFVMWMIHNGMKCRQ LDTCHCRHGTCKDSICPGLEES PLP
14706	45074	A	14792	240	771	GRGMQSPAQVDPAAKRGNIAG HTAHLWPKGGTLP LCF/YHLII MQIREQP*SSLEYPTF/RILSLVS GTKLNKILANRIRQHIKKLIHHN QVGFIPGMQGGLP TPGSEQGHL RVSPSSPSTVTLKLFNFMEPFE NLNL SKGKASVHTITQENTDSL KVQSGQFSQGHEKRTLDLKV S
14707	45075	B	14793	1	1557	
14708	45076	A	14794	150	1668	ESDARQGGPFPLENT RPHPSCMQ NHGICRSLHPGLCGCPPTARDA APATAGGVPAY/GPLTGAPPG* LPGAGIGSKQSSTMGPSGAGSC LGL*APSQPAD/PGSIQGVLVIA DTE*PLVGGDGGLEAEHQWQ* EAGP/GGLIPKHMNPQSRQQSLF GRRGYRDSSLRSVLGRTGQQT* HAELGAGVMGPGNGR*GH/G PRGLPCLVQGRRGPGVA AVAA GVSVAVPSGMLSENGPGCSK/P HSGDAGQRRGLREN L*GVRALI WGAASSFLLTEQDLQELADCL HSGRKTCCFFYFQGRGDVAPGPV APAHHRLAGISTVVP EGPGLCV GEDRQLPG/GNQRAEPPP*LVRS VSSLTGLPALGPRQMPNAGAG NGSGK*RGVRGSGPDWDCTGT HGGAGTGKLLWAGLSLFFPLSG KSEAHQRAAGHGYGRGLGSP GRPPRSRKGRVLGSESA PA*GSP QPLRSARQPESSCPRQQQPVG RGPAGPLEAGHCSFPRPLGP AR SLHPDFPQGLQA
14709	45077	A	14795	3	374	RRPPSWG*RGCSQLPECAADGS LEDHGLPPMVSCFSRHPAGRF LRVFPPSPLLA VDCCWHNNSYV VAVDCCSATCSLLLYPSQEFPP HKFLVYLVLSWHQLLGGLELIC TQQPVNPVVS DG

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14710	45078	A	14796	73	890	MSLVRTDGKVSFPHSRAASSPP PRFAGSLPWTPKKGHGFTSFPR EGYCP/REGPSDWGRNSFRVSS WAWRPSQGVSHHTPGQGP/PSP GNRDK*VATRKSPGQPGSSPEP GWSLQSTSSPGATRTKGNLNTL KG*KQVVD*WVGVTGWEGS GAQSPQPSREWLSRPGVGVV KETWSPSPWSGR*APPCGQPQG QQTHMERGGR*G*QVGACGLG P*GQWSSVTNGKDTAPWSPPP RQRNGRWPAPPPFTFHYYYYY YYYYYYYYFFFFGE
14711	45079	A	14797	273	678	TEESTSVLSVPNQTGAGAAIRGI VSLRLCGLYVTSPRAARMHIR PHGPWPGGSHHENGEGAPES/E GAPASASGRGAPEGQAWPPRD AVLSSLMLALFRTKSARHLVLG TRQTAASPPFFSQPSWYCSLG VDGG
14712	45080	A	14798	551	743	PTRITRSAGSSSWGSCRPRAPAP FSWSRPLCQGPGR*CRGLHSRF YAAP*VQGHVPVHILPYSKFRRG RAALRPRGQWGLDSVLGTAVC GCGP/RSEDICSGR*GPE/WYIS PPVPPHVHRGFQQLNCARQVG KGGGGPGCPMLGNHSSQVGL GLGGQDQDSLESPGRVSSPSGP SAASDPGG*GFQGNPDVHPAP APPDW

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14713	45081	A	14799	705	2299	KREWRPRHHPLGPPPRCAGRSA PLSGPASPPS*WLPFGHGPCGR MCSRAARGGDVTYRTHNTRAP SCPSLHWVGERG*DAHTRTPSC PSLHWVGERG*DAHTRTPSCPS LHWVGERG*/GCPHSLQLSFP PRSAGCCKALFEAEKSKGDTGL GKRGWAGGGAGGAARPCICNP TVPCPQSTQSPPV/PPGTR*QLG SSASHSRAASSPPRFAGSLPWT PKGHGFTSFPR/GGVLPFPEGP SDWGRNSFR/GPAGPSMW*PAP PSDAQVGHGPRAGLQRCRGR GGHTPFVAAAAIDSAYFS*/D P*VFGSNFPHLSCFP/GCGEGN Q*ARRRPLAGAAALPGPNLES WVCELSVAGPAVWDPVPSP/GD PTTGPEP/RNSAGACGAQGS R*T*GTPATWSL/GPPPELPGSR HQRQCECGPAHVQREMPGW ACMLKSVAQRGFQRR*QLSKA QAAAWRV/PGGR/GAGKD*GW RRWGVSRGGGGLCCARGGGGS SVRRGEVEGS/GCARGGGGCAG WRALSPSSLPSGAQELGS
14714	45082	A	14800	1	267	CSAGGPWRAPQPRRFHRRRP AQLPPLPLPPLPASPRIHNRFT PRPSQRTPPPAALGCPEPGS/RS QGRGHARPPGSGEGDPTVSSPG
14715	45083	A	14801	218	430	
14716	45084	A	14802	9	201	
14717	45085	A	14803	1453	1936	EVEKHLCCQ*ELLRAQH*AA ACRRPRPPAPGPQCSAGGPMAR APAPQVPPPPPPCSA/PPPLPLP LPAS/HAHPQPHFRHGRSALLP RPPWAVRSRGALAGPRTRAA GLRGGAGAAPAPADARFPASSP AE*PKFPQNSARALTGFPRCTD PTVSSPGY
14718	45086	A	14804	1	580	TSGCSHSLHKPAGVSTRPTVA SICAPRPTSLRRGLTLWPF GGHLTLLET/PGFDSCEVEEGP RFSTFKTS*ARGRRQRCA RREVGPSSAESGRARGEP RLLCRGGK/DPQPRAGEG GTPEGRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR CWVGEPPGRRTRLFPDE

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14719	45087	A	14805	279	1148	ALHEFAMSRSLHASLH*S**STC P*QQPAPAPAGEPRARFPKGSSS ASSGPG/WPRNHGKQLHLPAPQ Q/QQGRISPRVAGSGCTGRA LLLAAGLQNSTRSLNPRDPPTIL SHRPLQGM/PDAP/RGCSHSLHK P/SRS/TPLSGQL*PPSAPHAPQ APSVAGPLPCGLSPGDT*RYWR LLRFDSCPEEVEGPRSTFKTS* ARGGWRQSRVWASARGASTL QASVQGR*NQPRAGEGEEAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR FLGGCLL
14720	45088	A	14806	765	4270	SQDTPGDLQCHGDDL*DGAVLS EAPGGERVPRDD*GGVCEGVP HVSLRLDSVAEALQPRGEAGG DQVPEAHARPPSAQR*PAGAGL RLHPPAAGGVPGQSGGHLPKIQ DDLTSKS*TNSTKTLFPNKVTL SDSGRA*ILEGHRSTQGSLGLEA DPGTVSHHQPCPPNAAATHFF HRTARPGVQQGPGPASVQQPES DGDGALLRSPCSLLPQGADEVL LQPDGDKQGGPRGDSSESD*G YSERR*AQDEYQGH
14721	45089	B	14807	133	2943	
14722	45090	A	14808	1	814	MEEELLRELLYSENWWSIPYND TIQELCCWAVLKRTFINGNTSR KPGMKMVTGLKKQERRSKQW GCEKEAKFVPMWVILEVGR EERGIDGKRWGKSCSVESQSVW AFQNPWSKAQTLNLSMK/AYE KGKEGVEEKFEARRSWFMRKK AISHLHNMEMQGEAASADVEA AVSYPEDLAKIHDESDYTKQWIS NVDKTVFYWKMPSTRFIATE EKSMPGFKASKDSLTPLLGTNA AGGF*LKPLTTYHSQTSRALKN YAKLTLLMLYKWNK
14723	45091	A	14809	123	515	PKQSAKTIWTSARPEDVVTCS FKEEFLPGNTHHDFSINKRSDPE LEVSRPLARPENFPANRSHSLE L/RPCRGRWAAHWTCSSLLD ASSAPRTDQPSLWRNLPTASLG GPWSHNQPGIVFQNTYLMKW

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14724	45092	A	14810	279	1136	VDDVLCACVRGLLSCDEFLSW LALNRTVLATPALPSCLSQMAS SLPGLCARTRRGERADSQRGTC AFFSPARTASQAPLVASSVRKQ RVWAPNPLNCHTLPPSRGSQRG GYIGEEGVFGSRVVGIVVPGPN GSPWPLGVQR/PECVLLGVGSG S/SSHELFEADFISRLLAAPSPSP APAS/MGNAIEFEAPELGPLGRV FVDDFHYDYNFIHLHEDLCYGP LEGPDLDLAGTGDRTPPLHSRP RASLSPSALRCP*ALGF/WTLA WGSPNSSSRVPEAQPPAPSLAE
14725	45093	A	14811	1	1597	GGRKAAVGVETRPQGSQAQPTW LPVHGDTCITLLPCRAWWRL GGLPWAASVVGAKCVWTPPER GLLMLHKPMFGWSSGYRVVLP AVAFFRLRAQVTKLGEVSLRF LKREAKLCGFLQKSFLALEKR MKASESSRLKLEGSRLGELES WEKLRGLMEERLALQGQHEE SHLLEQCQGLDAAVAQLTKFV QQNQASLNRVLLAEKAWDA KGRLEESRAGELAAVQENLE AAQLAGELARQEMHGELVLLR
14726	45094	A	14812	150	1625	CLGKAFSCRELNAYLRLPTFFIV FSLRQPSLRMHSAWVVKTCGA MPCSCCRRHCSSVTDMAVRSL ALLQLVNRTPLRRRQISAACQR MSTFLFFRACTF*PRNRSSGRH /DLTARPRQAILRQNFK/RAQS RNLTA PNSPR**LLVKTYRQTS RPVSAAH*CPR*RGRAALAAAC HSGSPGARQTAGPAEGPAR*T RRDFL**RAACLRRRWKWP* L*RSRSSP*SQGSCPPALPAPRR CSAGSRTGPAARWCRAGAGSR RHAGSSA***SRR*GRSASGRR PRHGGTAGSGRWLWWARCPA *AGIPWSPWCHSSWP/PQSVRV VSSG*RASLHSPGLDSSGGGLQ SFLLVQLPAQKKTSSQP/RHAA APSAACPHAE*CTLGSCPRSA TLSPTPPRASPPAG/RSVSPCPP GHEGVLVISKHLLLSRSRGRG LGGNVVRPCSVQPMDGVGQEL AVADRDQLPCLVCQDGECPLK ASGRPVLGCP

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14727	45095	A	14813	921	1446	ACCISHGNLWHHLDDQKHGLQS *GEKSRLFSRPNLQVPVHTGLD HRARYLTGPRKQGHLLWPTGPS SVFDNENFCKLSVGM*TRGRASA RQQIQSPFAESGKAFFDICSVSL RLCVLPHPWNSRLRSPALRNSL KYSVTSSAAARRKLLPLASGPL RLGPRSLPTRLQVLRWEKVASA
14728	45096	A	14814	1	675	
14729	45097	A	14815	1	2341	MASDLVNRCEACDLPGQPISVH QFPRLSNEVTTTVGRNSESPNQ RSVSGPWTPREVRRGVAAAH GFSGQNAKWAAHIPATAMSFA LPYSLVHSPHALTTTHPLNPGDA VTMPSWTSTVSAANASKGRSFS QCFQSTEEGQERRRPRTSQAKV QQGSTAGKYNELITLAGHIKSQ APHGKRKPPRDSHVICSMLRK RKPDETPSPSSDAQFSGMLAVA VSSLLCPRSSPSQWCHCHSPSTT ILGSSDVSDTSFQPSTKLGPVHG FPPQSRDCILDFELIRKVTGAWS SLTAGSWETKIQEFSEEDILAPH RITPGPHSSKSPVHFLASLWGR KTKLYHHTIQDKEPRSVPEAGS SGRRDGGGAHSMCLMAPEPD HPGSPNCRSPATLHADADGN LQREAAKCGDGTQVSTHVDH TSAPRQAETGPA TGENEKMESH GRSKRGLVGADQCPAETLDSY TLLVGHKKRDKDRQTPGPAPQ VNSFVPENYLLRGPLAPLGSAIS MKTAGA VHIRPSGDLGRAPAP AVRPRPRPRPRRLLPGPAHL GAPRPPAPAPLSRRAARQSPAA AAAPPPGCE/RRG/PAGPASGAG PPAPAHGARPGGKPAANPPRAP QP*P/RRRRSRRAQPRPGPAPL SRMRAEGPARALRPPPHYQPEL GPPSETVGPVTELLAPIPTARFP TRSHYPVVTASPARSS*TSGLD*
14730	45098	A	14816	44	455	HLNRNR/PSQ/TPHIYNHLIFDK /PLFINIWWENWLAICRKLKLD PFLTPTYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP

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14731	45099	A	14817	1	279	IQDIGMGKDFMTKTPKAMATK AFIDKWDLIQLKSFCTLKEITIR VNRQTTENYPSPDKGLISRMLP NF*RLFPAS*KKPPLFDIGKTEK TNY
14732	45100	B	14818	1	2025	
14733	45101	B	14819	1	3570	
14734	45102	B	14820	1	1380	
14735	45103	A	14821	1391	2742	KKRESSLTHVMRPASF*YQSQA ETQKKRILDQYP**TLMQKSSI K/YLAKRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHMIIISIDAEKAFDKIQQPF MLKTLNKELEETTvkfiwnq KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSL FNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIFTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYA AKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAI IKKSGNNRHAPFSIH THIMFGSLYLQIKDLSILGFW YPRGILEPT

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14736	45104	A	14822	1	1698	MEDEMNMKQEGKFREKRIKR NEQSLQEIWDDYVKRPNLRILIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIQIEIQRMPPQRYSS RRATPRHIIVRFTKVMKEKMS RAAREKEIQTTIREYYKHL YAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAIFYQRQSESI MSEFPPTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTIFFTELEKTI FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDLP FLTPYTKINSRWIKDLNIRPKTIE TLEENLGITIQDIGMGKDFMSK TSKAMSTKAKIDKWDLIKLSKF CTAKETTIVNRPQTKWEKIFA TYSSDKGLISRIYNELKQIYKKK YTNNPIKKWVKDMNRHFSKEDI YAAKRHMKKCSSLAIREMQIK TTMRYHLTPV
14737	45105	B	14823	91	1596	
14738	45106	A	14824	1	2757	

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14739	45107	A	14825	1	2677	MGKKQSGKGTGNSKKQSA PPP KEHSSSPAMEQSWMENDFDEI NKIDRLRLARLIKKGKKNQIDT TKNDIGDITTPTEIQTITREYY KHLTYTNKLENLEEMDKFLDTY TLPTINQEEIESLNRTITGSEILAI INSLPTKKSPGPDGFTAIFYQRY KEELVPFLLKLFSQIEKEGILLN SFYEASIIIPKPGRDITTKENFR PISLMNIDAKIFNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIR KSINVIQHVNRNTRKDKNRMISID AEKAFDKIQQPFMLKTLNKLGI DGYLKIIRAIYDKHTANIILNG QKLEAFPLKTGTGQCPLSPLL FNIVLEVLARAIQEKEIKGIQL GKEEVKLSLFADDMIIYLENPV SAQNLLKLISNFSKVSRYKISVQ IPQAFLYTNNRQTESQIMSELPF TIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTKKWKNI SWAGRINIVKMAILPKNWKKT TLKFIWNQKRARIKSIKSNQKN KAGGITLPDFKLYYKATATKTA WYWYQNRDLQWNRTEPSEIT PHIYNYLIFDKPDKNKQWGKDS LFNKWCWENWLAICRKLKLD FLTPYTKINSRWIKDLNIRPKTI KLEENLGITQDIGMGKDFMS KTPKAMATKAKIDKWDLIKQE SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYSELKQIYKK
14740	45108	B	14826	1	1186	
14741	45109	A	14827	1	2304	
14742	45110	B	14828	1	2995	
14743	45111	A	14829	1	3095	
14744	45112	A	14830	1	3654	
14745	45113	A	14831	1	3189	
14746	45114	A	14832	1	2064	
14747	45115	B	14833	1	3031	
14748	45116	A	14834	1	3192	

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14749	45117	A	14835	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRLQRLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSAAPHHTYSKIDHIVGSK ALLSKCKRTEIHTNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYVWHNEMKAIEKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQETKIR AELKEIETQ
14750	45118	A	14836	1	3144	
14751	45119	A	14837	113	1336	PTLAGTGNETSHLGFNAIPIKL RMTFFTEL/EKTTLKFIWNQKR ARITKSILSQKNKAGGITLPDFK LYYKAIVTKTVWYVYQNRDID QWNRTEPSEIMPHIYNYLIFDKP DKNKKWGKDSLFNKWCWEN WLAIRKRLKLDPLTSYTKINS RWIKDLNVRPKTIKLEENLGN TIQDIGMGKDFMSKTPKAMAT KDKIDKWDI.IELKSFCTAKETI RVNRQPTWEKIFATYSSDKGL ISRIYNELQIYKKKTNNPIKKW VKDMNRHFSKEDIYAAKRHMK KRSSSLAIREMQIKATMRYHILT PVRMAIHKSGNSSRSNIVHSVT QANALESSWIPFLPHIQYISKP QASSFKMYHVTDPILPPSSQHL DQAAIINLCLQWPLLWFECMCP SKIHMLKLTPQ
14752	45120	B	14838	1	3127	
14753	45121	A	14839	1	2742	
14754	45122	A	14840	1	1998	
14755	45123	A	14841	1	3030	
14756	45124	B	14842	1	2558	
14757	45125	A	14843	1	3828	
14758	45126	A	14844	1	4134	MRKKQSRKTGNSKKQSTSPPPK ERSSSPAMEQSWTENDFDELRE EGFRRSNYSKLQEEIETKQGEV ENLEKNLDKCITRITNIEKCLKE LMELKAKARELHEECRSLRSRC DQLEERVSVMEDEMNEKMQE GKFRERIKRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLARQANIQI QEIQRMQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSQ
14759	45127	B	14845	1	3555	

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14760	45128	A	14846	1	3345	
14761	45129	A	14847	1	3451	HTKNPSVHHHRQRPKVDKTTK MGKKQNRKTGKSKTQSAFPPP KERSSSPAMEQSWMENDFDEL REEGFRRSNYSELREDIQTGKG EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRN WIKSQDPSLCCIETHLMCRDT HRLKIKGRRKIYQANGKQKKA GVAILVSDKTDFFKPTIKRDKKE GHYIMVKGSIQQUEELTILKIYAP NTGSPRFMKQVLSLDLQRLDLS HTLMGDFNTPLSTLD
14762	45130	A	14848	1	2606	MVASRSSRVGVFYGGQNSVDG VSRSSDGLNELCLYRPPTGAY LAYDTLDVLPSGQFTVNTPPID VNGKSLALLWEHTSLLTSMG GGRWAMQPLGLGLEHLGD RRDQVLDRSGRSRLDAQAHL RHRPDRRQGMVGVLTNQKEP RTRWIHSRLPEVQGGTGTVPSE TIPIDRKEGILPNLFDASIIIPK RGRDRTTKENFRPISLMNIDAKI LNKILANRNQQHIKKLIHHDQV GFIPGMQGWFNICKSINVQHIN RTKDKNHMIIISIDAFAFDKIQ QPFMLKTLNKLIGDGTYLKIIRA IYDKPTANILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLR AIRQEKIKGQLGKEEVKLSLF ADDMIVYLENPVSAQNLLKLIS NFSKVSAYKINVQKSQAFLYTN NRQTESQIMSVFPFTIASKRIKY LGQLARNAKDLFKENYKPLLN EIKEDTKKWKNI PCSWVGRNI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLHY KITVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNLYIFDKPEK NKQWGKDSL FNKWCWENWLA ICRKLKLDPLTPYTKJHPRWIK DLNVRPKTIKLTLEENLGNTIQDI GMGKDFMSKTPKAMA AKAKI DKWDLIQLKSFACTAKETTIRVN
14763	45131	A	14849	1	2862	

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14764	45132	A	14850	1	3724	MGKKQNRKTGNSKTQASPPPK KERSSSPATEQSWMENDFDEL EEGFRRSNYSELWEDIQTGKKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSADEDEMNMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIQENFPNLRQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14765	45133	A	14851	2	2375	
14766	45134	A	14852	1	2376	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQAIDLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIL GSKALLSKCKGREIITNCLSDHS AIKLELRKIKNLQNRSTTWKLS NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKIEIETQKTLQKINESR SWFFERINKIDRPLTRLIKKKRE TNQIDAINKDKGDIADPTDRQ TTIREYYKHLNANKLENLEEM DIFLDYTYLPLNLQEEFESLNRP ITRSEIVAHNSLPTKSPGPDGF TAEFYQRYKEELRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWSVGRINIVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARIKSLSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWYRTEP LEITPHIYNLIFDKPEKNKQW GKDSLFLNWCWENWLAICRKL KLDPLFTPYTKINSRWIKDLNV RPKTIKTEENLGIITQDIGMGK DFMSKTPKAMATKDKIDKWDL IKLKSFCETAKETTIRVNRQPTK WEKIFTTYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAACKHMKKCSSSLAI REMQIKTTMRYHLTPVRMAIK

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14767	45135	A	14853	1	1576	MDKFLDITYLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSQYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKFIWNQKRARIKASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNILIFDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFLLPYTRINSRWIKDLHV RRKTIKLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLSFSCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYA AAKKHKMKCSSLA IREMQIKTTMRYHLTPVRMAII KKSGNN/R/CAPGTPERQNHLS WKG*SQEPSGLAQWIPLWSP AS*DPLA*NSCCQHSCLKSTWD AQACARKLRTLIGYRNCQLE
14768	45136	B	14854	328	1467	
14769	45137	A	14855	3	3412	
14770	45138	A	14856	1	2907	MDKFLNTNTLPRLNQEEVDSL NRPTGSEIVAIIVNSLPTKKSPGP DGFTAEFYQRYKEELRIKYLGI QLTKDVKDLFKENYKPLLKEIK EDKNKWKNI PCSWVGRINIMK MAILPKVIYRFNAIPKLPMTFFI ELEKTTLKFIWNQKRALIAKSL SQMNRAGGIMLPDFKLYYMAT VTKTAWYWYQNRDIDQWNRT EPSEITPHIYNILIFDKPEKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLLPYTKI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
14771	45139	A	14857	1402	3004	TEPKTKTT*LSA*MQKGPLTKF NNPSC*KLLIN/IVLEV/LAIRQ EKEIKGIQVGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNILCSWVGRINIVK MAILPKVIYRFNAIPIKLPMPFFT ELEETTLKFIWNQKRARIAKAIL SQKKKAGGITLPDFKLYYKATV TKTAWYWYQNTDIEQWNRTEP SEIMLHIYNLYIFDQPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKLEENLGITIQDISMGK DFMSKTPKAKATKAKIDKWDL IKLKSCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELK QIYKIKTNNPIEKWKDMNRHF SKEDIYAAKHKMKCSSSLAIR EMQIKTTMRYHLTAVRMAIHK SGNNSLIVGASMDTSLSGPIPY DIQHDFRFGSVTVRRGCAIEFY

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14772	45140	A	14858	884	2925	GIKYLGIQLTRDVKDLFKERS/Y EPLLNEIKEDTNKWKNI PCSWV GRINIVKMAILPKVIYRFNAIPK LPMFTFFTELEKTTLKFIWNQKR ALIAKSILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI DQWNRTEPSEITLHIYNLYIFDK PEKNKQWGDLSFNKWCWEN WLAICRKLKLDPFLLPYTKINSR WIKDLNVRPKTIKLEENLGITI QDIGMGKDYMSKTPKAMATK AKIDKWDLIKLSFKTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYAACKHIM KKCSPSLAIREMQIKTTMRYHL TPVRMAIHKSGNNSPTCVSQD WKLTAQVGLWSAEAEAPKSAQ RRPLAEGHRAAVQRDGSGLQL LCTVKLQVLPCHIAQNGGRKA TSSLEAELTSWRPLCLEDGTGF RGEDTLETVNAEGRENRRKAG HRAAGSSASRRCRNTGRSVQRL RPQKTQAFPTHCHFCILVVK TQLNPKSRVRKVPFAPMKHKG ALAGPWANICAGKSSNEIRTCD RHGCGQYSAQRQSRPHQGVDI LCSAGSTVYAPFTGMIVGQKEP YQNKNAINNGVRISGRGFCVK MFYIKPIKYKGPIKKGEKLGTL PLQKVYPGIQSHVHIENCDSDDP
14773	45141	A	14859	1	2577	

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14774	45142	A	14860	3019	5574	RÉTRGEVKNKSNQSTAPPKDC SSLADPKKIQTITREYYKHLYPN KLENQEEMDKFLDTYTLPRLN QEEVESLNRPIGTGEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL VPFLKLLFQSIEKEGILPNSFYE ASIIIPKLGDRDTTKENFRPISV MNIDVKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFIHHSI NVIQHINRTKDNHMHIIHAEK AFDKIQQHFMKLTKLNKLGIDGT YLKIIIRAIYDKPTANIILNGQKL EAFPLKIGTRQGCPLSPLLFNIV LEVLAIRAIQEKEIKGIQLGKEV VKLSLFADDMIVYLENPIVSAQ NLLKLISNFGKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLEIKEDTNKWKINPCS WVGRINIVKMAVLPKLPMTFFT ELEKVTLLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYKYAT ATKTAWYWYQNRDLQWNRRT EPSEITPHIYNYLIFDKPDKNKQ WGKDSL FNKWCWENWLAICR KLKLDPLFTPYTKINSRWIKDL NIRPKTIKLEENLGITIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKQESFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYSEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAANKHMKKCPSSLA
14775	45143	A	14861	1895	6140	
14776	45144	A	14862	1	2875	MKAIEIKVFETNENKDDITYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDTLTSQLKELEKEQEQT HSKASRRQEITKIRAELEKEIQTO KTLQKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITTDPTIEIQTITREYYKHL YAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPIGTGEIVAIINSLP KKSPGPDGFTAIFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
14777	45145	A	14863	2843	4460	HQHQQKPHPHRNPIQKSPTSST KVLVLAIRAIQKQSGIQIGS QEVKLSLIEDDMIVHLENPIISA KNLLQLISNFTKVSQYKINVQK SQAFPTYNTKTQIENQIMSELPFT IATKRIKYLGIKLTROVDLDFK NNYKPLFKEIREDTNKWKNIPI SWVGRINIVKMAILPKVVIYRFN AIPKLPMTFFTELEETTLKFIW NQKRARIASLSQKNKAGGIT LPDFKLYYKATVTKTAWYVY QNRDRDQWNRTEPSEIMPHIYN YLIFDKPEKNKQWKGDSILFNK WC*ENWLTICKRLKLDPLTPY TKINSRWIKDLNVRPKTIKTLLE NLGITIQDIGIGKDFMCKTPKA MATKAKIDKWDLIKLSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHKMKSSSLAIREMQIKTT MRHYLTPVRMAIKKSGNNRC WRRCGEIGTLLHCWWDCKPVQ PLWKSVMRFLDLLEIIPDPPI PLLGIIYKGYKSC
14778	45146	A	14864	1	8335	MGKKQNRKTGNKMQSASPPP KERSSSPATDQSWMENDFDEL REEGRFRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSADEMNEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDIQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIRTLHPKSIETFFS APHHTYSKIDHIVGS
14779	45147	A	14865	1	3166	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDISRTLHP KSTETVFFSAPHHTYSKIDHIVG SKALISKCKRTEHTNYLSDHSA IKLELRKLNLTQSRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYQNLWDAFKAVCR EKFIALNAYKRKQERSKIDTLTS QLKELEKQEQTHSKASRRQEIT KIRAEIKEIETQ
14780	45148	A	14866	1	3912	
14781	45149	B	14867	1	2832	

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14782	45150	A	14868	1944	3531	LRDCKRINQHPVKTDQSAFCM/AP/MQDQVVLARAIQKEIKGIQLGKEEVKLSLFADDMI VYLENPVISAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRIINVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARMASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNLYLFDKPDKNQW GKDSL FNKGWENWLAICRKL KLDPLTPYTRINSRWIKDLNV RPKTIKLEENLDITIQDIGMGK DFMSTPKAMATKAKIDKWDL IKLKSFCIAKETTRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYA AAKKHMRCSSSLAIRE IQIKTTMRYHLTPVRMAIHKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCCMRKNKTLI
14783	45151	A	14869	1182	3891	KMIKGISTDLTEIQTIREYYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIGTAEIVA IINSLPTKRSAGPDGFTAIFYQR YKEELVPFLKLFQSEIEGILP NSFCEASIIIPKGRDITTKENF RPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFN IRKSINVIQHINRAKDKNHMISI DAEKAFDKIQQHFMKLTLNRL GIDGTYFKIIRAIYDKPTANIILN GQKL
14784	45152	A	14870	997	1161	CTSTVIMSICTKLQNKEHVJEA LRRAKFKFPGHPKMHHSKK*DFT KFNADFED
14785	45153	A	14871	1	1458	
14786	45154	B	14872	53	1468	
14787	45155	A	14873	1819	2235	

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14788	45156	A	14874	707	1613	VRARAGERARVVRENGKAELP VALVLPRLSHTFTCTDLKVQ FHQRLRLQEKSGKFIGSNMSQE SDNNKRLVALVPMPSPDPFNTR RAYTSEDEAWKSYLENPLTAA TKAMMSINGDEDSAAA/HRPAL *LLQENQSEPIPREGVGWG*GE ER/ERMTEEEQEGEGGGGGRGG GEGEEEEEEEDVEEEEEEEEE EKEEEEKGGKEEENEKEKQR EGRRGKETSNQGMVRPRLLP HQEHSRNYLVFIMDSNMIEICF REASISPKAQAYVLIPDFKNCIY GWEDSIEILWGLPGSHVL
14789	45157	A	14875	3	346	QRSKCKVPLGKPLTLPPKPE KVPQGQKDRRPTGFKP*N*RRRR SEKSLRFFPPGS/PQAVPIPVGFS FDTNL*HFL*KPLIFIMGTVSL PHPRSPSAPPPTPQRPMTFCHLK Q
14790	45158	A	14876	1868	2666	GLLLSPFQGLQGVAPRKTRSNL HPGSLAHLSHQPPAPWPPRGLW PPGQETSCHCASGRALGTGSPR PPHAPWLHLEPQRAHSGAPSP GSSPSAPLHIPVAPENQLSLGHR SPPNPSPGDCYPSPSGP/PPSSLD SPGLQTAPGAMFLSPRSVGQSA CPTPRSLDLRNSPASTPDQSVCP TPLSLA WLWPPPSPTSAKSLIFT LTSEVQSFSPPTIPPGSSDPPLSK QP/SGSCLSSSGHLTSPSVPRHSP WPRSSPQNPHSWTLPS
14791	45159	A	14877	762	1528	AIPGGAA WPFRAEGAQGFGKR LTFKPLGAQRQSVSGSEVPPL PLHLKMAPEMPVAL*SPGTGV HPSLLPPT/GPKVPPGRIDRGVPV TLAPQVGTAPIQWHCRGSRCP G/SRPPGGWR/RPCQAPAPPLGQ HLPRLLPPTPGQGRPLTPSEP PPWSCWLPASPPAGPSRRVGG GPGTCQGLLRS*GLLLSPFQGL QGVAPRKTRSNLHPGSLAHLSH QPPAPWPPRGLWPPGQETSCHC ASGRAVGTGSRPRRA

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14792	45160	A	14878	1	963	MARKDCCSPGDSSPGRLPLVL PAQCLVLLRLQITAFSSIHVAAN DMMSFFLMAKQDSIAKYRIFF IHSSVDGHARPLSPSLVVENG GKQVLLCSDNASPEVSTVALA SCPGTFPRHCGAAESTHICATG LGELTPQGGHGHIPNKLACCAT GLEELVPRDHGKLGISWFGFIA GAYLNLARVVGECQGSYGYS LHHYCYHYHYHYCHYHYHAA TY*NHYHYHYH/HNNNSYHHH SYHYHYHYHYHYHYNCYHHH YHCRHYHHPHDYHYHYH/RHY SLYYCIYLCYHYRYCYHDHSS HQHNHHECLP*VRHSAEHLQY
14793	45161	A	14879	105	1448	CHQPPASPFSRREFGGSEKPPER GCPAWEPAAGPVQPLGEDGP RLCQPPPPSPDHALG/PYGHQRS GRPTLPGRPK/PAKKRGR*PSS TGQ*SHRPITGTGGQAGGSG* VTAGGQ*PPQNL*AKISCPMP GPSPGMQQGVKHPSLFSHQTV AKGFTTRWNCRQVCPHRGERK WISSVRPCGGALAPSCA/DGLR GRRTLSGSQPLW/PPAAVSAVG QLQPPCHTLTPHPLQNSTQHAE PQRGSVYSL*EGTSP/LAAVPFA PHIEKRFSTFPAGDA*PSEAH/A PGPACCHSPGLEGVPSRAGPG TSAGR/PGNGRERAWPPHSGPS TPPDTSCG/SPGPQLARAGSRRA NGSTLPPTRQGF/LPGRKDSAGA CGQP/*AEGAAAGPSRPAER AVLPLPR/GRRKCRGGGPGVET GVSGARRGGDRSGCSPAALDA EAPASLAGVSIRES
14794	45162	A	14880	1	2421	

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14795	45163	A	14881	1080	2571	VHCRFWILALCQMSRLQKSPILL FNIVLEVLAKAIKQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI V/SAQNLLNLISNFSRVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTKKWK NIPCSWVGGRINIMKMAILPKVI YRFNAIPIKLPLTFFTDLERTTL NFCNQKRAPTLQVQSLSIQKN KAGGITLDPFKLYLQGLQ*PK TAWYWYQNRDIDQWNRTEPS EIMPHIYNLYLFDKPWEK/HKQ WGKDSL FNKWCWE\NWLAI CR KLKLDPFLTPYTKINSRWINDL NVR\PKTIK\TLEENLGITIQD\IG MGKDFMSNKT PKA\MA\TKAKI DKWDL\KLKSFCTAKETTIRV NR\QPTKWKIIFTYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSTSLAIREMQIKTTMRYHLT PVRMAIHKSENSRCWR
14796	45164	A	14882	136	420	RESRNL SRGEESDPAEPS\ RNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPSPAPPETHTGSPRPPSGRSR IRAYLH
14797	45165	B	14883	1	1197	
14798	45166	A	14884	3	538	GAGTDGGRTPAPRAFDPDLGEA RTSAPTGPARP GGSASAARPA VRPAEPAAEETQEOPRAGKRAI HEYRYVYVQQRKTDPPQAV A VFGIPADGD*VSR TAYHAHQPL AWSGR/E*MCLSMAMWNT*ST MKK*ISIRVISRCSGPVHRTN*QI PEPVRAWRFLICRCICFSPGRWI KT

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14799	45167	A	14885	1208	2765	KMAPTWDKMVSSAQMGFNILQ ALLSQLSQDELSKFKYLITTFSL AHELQKIPHKEVDKADGKQLV EILTTHCDSYWVEMASLQVFEK MHRMDLSERAKDEVREAALKS FNKRKPLSLGITRKRERPLDVDE MLERFKTEAQAFETETKGNVICL GKEVFVGKKPKDNRCRYILK TKFREMWKSXWPGDSKEV/RGY G*EIQDADPIQQPQGASRALPY TVVLYGPAGLGKTTLAQKLMML DWAEDNLHKKFYAFYLSCREL SRLGPCSFAELVFRDWPELQDD IPHILAQARKILFVIDGFDELGA APGALIEDICGDWEKKKPVVPL LGSLLNRVPLCIENKLGVGGED WGDQLRVYWWNPSKREGGSG WSHGSEDANQSLKHLRLSANV LLDEGAMLLYKTMTRPKHFLQ MLSPWETTTLAQIIMLDWAEETS SDKLKYAFYCSCRELSRLCPCN FEELVFRDWPELQDDIPHILAQ ARKILFVIDGFDPLGGRTLWTL TRGHLRELGNRRKRCPSWGV
14800	45168	A	14886	213	625	EPGIDTSCLCAGRCRSPGKGRA CGGSSPCSWPGQPPAPPAAAV PACPSGGRGAGPIQSGTCCSR ADSRCSTWTAW/WPPGLGAAT VQTVMS*TV/WPMPHVPAQGW LALGQGAAAAKHPLTSATTRS WCLGVGPGPVM
14801	45169	A	14887	1	375	MCNAQVLEYMGKSSLLTSDL QLVRDALRSLRNSFGHDPQHH TIDSLQGISSLMERLHVMEQ KKQERKPPVIPRQT/VVWSGP PANSNRPAEPPDC*KEN*RDA LRSLRNSFGHDPQHHTIDSLQ GISSLMERLHVMEQKKQERKPP PLVIPRQTGSGVDLQQTPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL

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14802	45170	A	14888	1	750	MGELNQGSWRQGHLP.DAAN GIAIRVPRRRKDESRRKNPTRKPH SWKPTKNFEDDVEVMKRSMSI RIEDTHSGPSAAGVLEFAGGPL QTLFAWVSPAEEAEQQRLLPVP /CLWKLCPRGAPARCQRQNSPSK LPSTGFVYTVRGKLPQTQASVVVD APPATKLECPRSTSDCCAGSKN FKPVDLSLLASVGPVRNLLQVES SHYGKISVTVAGHCPHATGRI LGKQALRWSPMCSMFIGRALG LVPVEGGLLQIA
14803	45171	A	14889	81	164	VGKQGLEWTFPANSRRPAAEGP DC*KEN
14804	45172	A	14890	1	674	MVVYACSPSYLEAEVGGSLSE VEATNPKNSSKKFLDLSEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFYFGI YLTKEEERLKPSRKKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTPPLVIPRQ T/VVWSGPPANSNRPAEEGPDC QKEN*QTERNSINIKKDIHTKT PLCI
14805	45173	A	14891	619	931	YLLMDFLLHSWLVS LGDKVP HEFWRGCPSCSFGPRFWVAGV LVL*APKL*LRQVRSAGKRCGQ KW*IK*/SDRLCVD*NK/WSDS LKPATSCSLIVTCHSLLG
14806	45174	B	14892	1	658	
14807	45175	A	14893	48	288	LCSIKKPEKSLLCW*YPGNRVW SGPPAKSNRPAAEGPDC*KEN* QTERNSININKDIHTKTPSEGH QHQRPKTKPGRI
14808	45176	A	14894	801	1157	QSGPSAAGLLDFAGGPLQTLFA RVSPAEEAEQQRLLPFPSSGKL RPRGAPARCQPELSCMRCR*SL LGGVSGSYGMGVRDPFEEAAC PLSELECSAGRSALLRMVRQG HLGLLKLRP

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14809	45177	A	14895	1	1891	MPVWVTVVKSWNTQIGRPGH VSALGFELTKNPWPLTYESGDG RSLGKPGA VSRGRGRHGPHPQ QAECDLPAGRIAGPCERGLERQ EKLPPAPQGGAWHLRLSRERFK SEDAPKIHVALGGSFLNLAF LVNVGSGSKGSDAACWARGA VFHYFLLCFTWMGLEAFHLY LLAVRVFNTYFGHYFLKLSLVG WGLPALMVIGTGSANSYGLYTI RDRENRTSLELCWFREGTTMY ALYITVHG YFLITLFGMVVLA LVVWKIFTLSRATAVKERGKN RKKVLTLLGLSSLVGVTWGLAI FTPLGLSTVYIFALFNSLQAHKQ LKDRKVGPHFMQGA VFLEGGF WGVDIASFEPQEQFWWTNLGK EDEDKSFDMPHSWVEQIEISPEE EAMGSAQMVRGVSGPERGSKK RPQLTVSTAFETRCPNGKKVIQ YKRAKLEKWAPYLNNSGLVSR LTTYEDLQCTNILEIKWYQNR EDMLELKHINKTTDLKTDYFKP GHPQALRVHSYKSMQPEMDRV IEFYETARVDGLMKREETPRMT TEYYQGRPDFLSYRHASFG/RPS QEAHSEQCRVKPPAHCAKPAE DDV/RKSACFWSRRSASSCATT AVRTTSRPPSASSCGAPRWAK
14810	45178	A	14897	1	425	HVQQTETISRTVSTGSPILSCSVP VTLPNGPVLWFKGN/AGPNRKL IYNFKQGNFPRVKEIGDTTKPG NTDFSTRIREISLADAGTYVCV KFIKGRAIKEYQSGRGTVFVT VSYSSRSQKSEICISGLKSRHQQ NCSFWRF
14811	45179	A	14898	1	393	RQGNFPRAKQIGDITKPGNTDF STRIREISLADVGTYYCVKFIK RAIKEYQ/SGRGTVFVTEQNP RPPKNRPAGRAGSRAHHDHHT CLSALPERNSTNYFVQPCCLLR LLGLTGFAVKIIQTGKERTSK

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14812	45180	A	14899	1	753	MGSSLSPVLVYALPVRQPLI.RS VVEERSTKMRVSGPGFQAKFRF YSQGLSWSARGEGLVPFAFWL QPYPRPLNFKAEEMTEQKENQT YVDGGFRPYIHRRKNL.TEGHK AEKEMEPWDGFSDESCRTHCQ VHDYAKGHGEVQRERVDEQK EHLGRRRQDCQQHLNRR.LHC /TVSGEAPSEASGSVRGHGRAH GLAGSERHGHDAAPEHQLLQ SVDADHVVPVAVYQFWDDEG RGILSPGDHKKPDRRGAALY
14813	45181	A	14900	6	726	VEGISRTGIQAEQAPGFTTMP VSVNPGDVLTLACNMSALSPE GPVLWFKSIGPGQQLIFSCNGS HFPRVTPVENTMVDQTDYSIILS CSVPNLTPNGPVLWFKGTGPNR KLIYNFKQGNFPRVKEIGDTTK PGNTDFSTRIREISLADAGTYYC VKFIKGRAIKEYQSGRGQTQFV TGEYVSYTPYPLVYNS/PLWDE ASRGRSRQSQLFCSLHW*YPR KQDEWTSSKLQQTCCRVA
14814	45182	A	14901	760	978	KKLLLLLLCGIEWHGFSSDSGS GGWVPEG*K*GCEHELLPEDVP SCFGWAECWLVRRTLPLFHYV ELCYSFHG
14815	45183	B	14902	772	1165	
14816	45184	A	14903	1	2133	
14817	45185	A	14904	1	1311	MATTPGRALGSLLPITLLGLTA GQPFISLTGPSHRTSPGDSVPFN CTAVPFNSQDFSRDFNVTWLK DSDEHPASAQRLVPDNGGNDFI TSKAWVTLTRQDVSSEITCEVT HRAIAEPLKTTMNL.SQATRN DGTYSLEHTWQAEATLEEREF ACWVVHDEQPLKANVT.LQAQ VRRQGGKQSVQPYKLQGPLQR SEPGTRIRLT.YASSGFSTHQVTV TWLKNKHEL.PNPQTSVQYSGH TYNVTSSVLVPLMDDDV.FSHV VCHVEHKL.TWFFQKTTGLDQY L/QG/DP*QLCGH.LTLPSSPRAP PQLPGLQHP/VVFHSQVLL.FSCL VAVTCLVQRFYPQNVHLAWLE DCHTLKGTEQPTLKKNNDRSY TLEKLLLVNASVQGPVRLTLC MMEHEGQPPKRANLV.LSTAHH TAYKPIGSTESIMVT.MIITISQM

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14818	45186	A	14905	3	341	RRATRPGN*GGRHNAGRSSARL ETGRPAMAPQGRPRPLGCRTPQ HPGHWPSAPGLLPPAPGPVAG MTQAQRWCPEPDAHFLQYTLTY FVRHIPQLPKQTPHHYIATRLPC ATQ
14819	45187	A	14906	154	679	GVCCPLLGGVSS*ATWGS GTT* GGNTHLI
14820	45188	B	14907	1	2554	
14821	45189	A	14908	387	826	ARAACLPRGSARGTAGAGEEPP DPAPLHLRGEGPAP/HRPRSFRG MGWPAAPSTRSPST*RRCLPP RPRWSP*SHPGPRASARRLP*LS *RASRSSEAPSGSLGSAQGQD CSRTGTGFSPPAFSDGQQTTPP APSSVPTLNSLG
14822	45190	A	14909	86	2223	GQEPQVREQKACHHLGSSPPPS WEL*EQRPAGP*N**PSTLTGT GSTTT*QIRMKVN*MGN/DSPQ GKNTPKMYSGEFSPPVRVHVFFS LSDLKQIKIDLKGFSDDPDGYID VLQGEDILAKAGAIRHLNIGEG THVCCPLLEEGINPEVWATEGK YGRAKNAHPQVVKLDSASFY QRQYPLRPEAQGLQKIVKDL KAQGLVKPCSSPCNTPILGVOQK PNGQWRLVQDLRIINEAIVPLY PAVPNPYTPLSQILEAEWFTVL DLRDAFFCIPVHPDSQFLAFED PLNPMSQLTWTVLPQGFDRDSPY LFGQALAQDLSQFSYLDTHVL WYMDDLLLAARSETLCHQATQ ALLNFLATCGYKVSQKPAQLC LQQVKHLRLKLSKGRALSEER IQPISAYPHPKTLKQLRMFLGIT GFCQIWINRYGKIARPLYTLIKE TQKANTHLVRRTSLOPVA YLS KETGTSLQPVA YLSKEIDVVAK RWPCHLRVVAAIAVLVSKAVK MIQGRALTVWTS HDVNSILTAK GDLWLSDNHNEEKIEHNWQQV IAQTYAAQGD LLEVPLTDPDLN LYTDGSSFEKGLRKAAYAVFS DNGILESNLTPGTSTQLAELIA VTQALELEGKREPNADNASY SCEPLEDLRLFRQPIEAVKLQ MVLQMEPQMOSMTKIYRGPLD WPASPCSNVDDIEGTPPKEISTA

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14823	45191	A	14910	929	1324	RRYQVQRPSEGLTVYLFWPV*/ PVVGVDWPLPTGPD\YSLLVPIPP PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPSPCTPMFHS PCSAMTAVTPSLARP*THGSP KAQGAQGVKGPSSGLEAPPW A
14824	45192	A	14911	2	286	
14825	45193	A	14912	220	249	P*N**PSTLTGTGTTT*QIRM KVN*MGN/DSQGNKTPKMY GEFSPVRVHVPFSLDLKQIKID LGKFSDDPDGYIDVLQ
14826	45194	A	14913	1	163	EPENPADNASYSCPELDRLL FRQPIEAVKLQMVLMPEPQM QSMTKIYRGPLDWPASPCS*DF LGRGAFNVINIGAWASRPVQGS AVDLSHGLHLGLHLKNNHL
14827	45195	A	14914	1	287	
14828	45196	A	14915	2498	2788	
14829	45197	A	14916	112	333	
14830	45198	A	14917	329	1666	
14831	45199	A	14918	1	756	
14832	45200	A	14919	1256	1651	RRYQVQRPSEGLTVYLFWPV*/ PVVGVDWPLPTGPD\YSLLVPIPP PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPSPCTPMFHS PCSAMTAVTPSLARP*THGSP KAQGAQGVKGPSSGLEAPPW A
14833	45201	A	14920	1	987	MLVLGYNRKNTTEGTQKQKGT NASDFHFLSQVLEQVSPKGS EAQCCVLRHLGCESESAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLGKERR QREGERRERKREKREKRESQR KERKREKKGKREKREKDRSDL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLTVWRDMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQA VP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPIN*SMIST ITQKKEENPTAFLERLREALRKH
14834	45202	A	14921	473	1015	
14835	45203	A	14922	3	937	
14836	45204	A	14923	530	612	LQAKVFFLLRWPAILRG*NYGP RGVPH
14837	45205	A	14924	101	430	

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14838	45206	A	14925	1	1587	MAALTLRGVRELLKRVDLATV PRRHRYKKKWAATEPKFPAVR LALQNFDMTYSVQFGDLWPSIR VSLLEQKYGALVNNFAAWDH PGDIVLDLCAAPGGKTLALLQT GCCLTWSRKCAALSMFSRPA RCLCRARTTAPRAVRRPDQRR ATAAATKQARATPEAPGSAA HSSYCTMIPSAACCI.PRLKPPH AQPARSAAKPLDQPGSHARL RGRGGEARQSLEAIRGPGSGIA PSDIPLPAKPSRRVIAQTYAARG NLLEVPLTDPDLNLYIDGSSFVE KRLRKAGIKAVKLQIVLQMEPQ MQPMTKIYCGPLDQPASPRSNV DDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLLTWRDIMLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAAP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKRKKPIN*SMISTI TQKKEENPTAFLERLREALRKH
14839	45207	B	14926	1	939	
14840	45208	A	14927	1	4317	MQSMTKMYCGFLDQPASPCSN VDDIEVKLEIMLLTERDDGKEV LDVGEERRYEIEEYDSK WTRK YNCLAVLRVHSGSQITTMKIL WYLVVALWCFKDGKIAASRS GGFSYGSSSGDLDRKKPLFSL EFGSPGETEDKSRQRQDAGSPK SEDTAGGFFNSSSSGSDSRTK PFFSLGLGAPGKAEDKSGDSQD AGGSKSEDTPPGGFFYGSSSSG DSDKKKPLFSFEFGATGEDEDK SRERWDAGNRSSEDS
14841	45209	B	14928	110	269	
14842	45210	A	14929	1	561	EVFPACSQLVYWGKPIITTYPLCE NNVYMLSPNASVCLYSPLAEQ FSHQFPSHDLPSVLAKFSLPVSL SEFRNPLAPAVQETQLIQMVV WMLQRRLLIQLHTYVCLMASP SEEEPRPREDDVPFTARVGGRS LSTPNALSGSPITSSDDMTLTSP SMDNNSAELLPSGDSPLNQRMT ENLLASLSEH

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14843	45211	A	14930	1891	2522	GLSNQNOQPGRCIPDAHPVQDI. VQDLVHTWCRVPCTSYVPCV* VPGAYLVHTRCIPGAGPGAYPV HTWCRTWCIPGAGFPAL/RPYH ALLLLSDEKSLLGELPIDCSPAL VRVIKTTSAVKNLQQLAQDAD LALLQAMGSAVALVMWAWP RATGPKLYCLRVGAGGACGWR PRLVAVSRALLVWRGSPWG PALAWQKSPEYSTKVLKQ
14844	45212	C	14931	113	274	
14845	45213	A	14932	1	1634	MEIPAVILTVAPILHLTSCGFV TGDGLKQAEKCAPEEWNPTK FIKLTNDQACFAGLWPLSEIQ RRTSRTVTIISRISALREKGNR KPTSISGSVNEMRQVLVKDQVS MPRVLPTHIFVPDEAGFSAGAV WPCAAPLWGSSWTPKVENCS FYIRLSFAISVGGDELKIAKLVS AFPERAYDLVGHQHQRPKVDK TTKMGRNQSRKAENSKQNMS SPPKEHNSSPAREQNWMENEF DELREVGFRRSVITNFSELKEH VLTHHIKEAKNLEKRLDEWLTR INSVEKSLNDLMELKTTTLREL EAYISFNSQFDQAEERVSVIDQ ISEIKQEVKFREKRVRKNEQSL QEIWDYVKRP/NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANIQ/QGKLQRTPTKVASSRT ATPRHISVGSPLNMKEKILR AAQRERSGLPTKGKPFRLTAAD LSAETSTSQKTEWGPIFNILKEK NF/QPRUSYPAKLSFISEGEIKYF TDQAKCLRDFVTTAFSCLP*K STRPALKELLKGST

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14846	45214	A	14933	1	1429	MVLAAGDPVEKGITWARENAG IYISCTMMKLSMIPIGDQSYRNL IPLKFVACILIEGNAKCWPLPEF DPSQIRLIVYQDCERRGRNVLF DSSVKRRNEDISVSRIKYLGIQL TRDVKDLFKENYKPLLNEIKED TNKWKNI PCSWIERINIVKIALIP KKLGSDAQVKVFGKCCQLKPG GDSSSLDSSVTSSSDIKDQCLK YQRTVDLSAQLSSSGKGQTTSS SGSLTPMTPHWEIPPSGGQQTSS HTGELRLASGRGSSGMKLPEEG TDRNLCCSAASSGDTQANRDW SGPPANTS RPAEAGPDCDRENG TKL.ENTLKDIIHENFPNIRQAN IKIQEIQRTRQRYCSRRAATPRHII VRFTKVEMKEKMLRAAGEKH WVIHKGKSIRLTVDLAETLQA RREWGPIFNVLKEKNFQLRISY PAKLSFISEGEMKSFPEQMLR DFVTIRLALQELLKEALNMARE /NR*QPLQKHM
14847	45215	A	14934	2320	2811	ESKLTRGVKDLFRENKYPLLNE IKRGHKQMEEHSMMLGRKNQ YREKWPYLPKVNL*IQCHPHQA TNDCFHRIGKKLL*SSYGTKKE PALPSQS*DKRTKLEASHYLT NYTTRLQ*PKQHRYWYQNRDI DQWNRTEASEIMPHIYTILILWT NLRKTSMGERHP
14848	45216	A	14935	2	872	
14849	45217	A	14936	769	828	
14850	45218	B	14937	1	669	
14851	45219	A	14938	1	807	
14852	45220	B	14939	35	212	
14853	45221	A	14940	235	837	QQAHKTPQRRHSAFTEYVRNN RLPETVIRVKQPALAIFSPDIAPL FVHFRADDDVTARVIAIIMIF WCDRVEKRVSDAVACFTLESEI AEVGVLCRTHIRQ*RVQVTPARM *ALSRLHACRSSEVVRHNRPPYP VIRVKQPA/RRDLAPT*PHCSSIS AQTTITSLPGCMREVTELRPEFF K*RKTVLRPTPIMRARAERRCK
14854	45222	C	14941	1	1755	
14855	45223	A	14942	1	747	
14856	45224	B	14943	1	2466	

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14857	45225	A	14944	1	333	LNLVLFQQRAELMIS*PQ*FSRA LLVIFPLLQTELQQLFLLHVN AAVEAPPSPVIGLYSENVRRNR LPETVIRVQKQALARFSPDIAPL FVHFRADDVVTARRVEKRCK
14858	45226	B	14945	1	1794	LNRRDSYVEYLADKVADREED AEEYLEAIMEARVTVAGMGLV MEVQDYDFDGEADRLAKAWLA EYTPQIKSLKDERKEAYRQIVE MSTEPQDQDLVLRPANKFEMTR VREGEKEADLPVWKHHL/SV*R KRELSGSVEPLGNQVFEIETKRE NS*EL**KSLKDERKEAYRQIVE MSTEPQDQDLVLRPANKFEMTR VREGEKEADLPVWKHHLCD SGNYPALLNHWETFLRSKPN VKIHRSSDKSPTYVFFISQYDL PAFYPIHGHLFVERVVKVRIVFI EEFADHHHLAIFQFNRLQRHA FVVTLANVTNQPFSSVVVVNL
14859	45227	A	14946	1183	1899	
14860	45228	B	14947	1	3099	
14861	45229	A	14948	1174	1545	
14862	45230	A	14949	1	945	
14863	45231	A	14950	62	576	
14864	45232	A	14951	1	1642	MLANIGFYNSNVIHRSKGAIGE GPPDPRGIVEQNLGGDISIPCYN GPPRRRSQAQKTTGLPNQPRIPS AQCAGAFPRVAAAGAGGGGG GGSGGSGFCLGWRLRRRRQRR RRWRRGEGEGDGDAGHMRPR PAGRAEARRRRRLRGNPPPGAR LPNREGNGSGVSWAAEVSGDG RGARTEAARTRRRPGGADNYP GAVPPVQLLTGWCVTAKAPPDI SAISALTAVKHGNCSSLTPLLNP PGSDVIVCAEMDEQWGYVGAK SRQRLFYAYDSLRTTVVAHV FGERTMATLGRMLSLSPFDVV IWMTDGWPLYESRLKGLHVI SKRYTQRIERHNLNRQHLARL GRKSLSFKSVELHDKEELAAL FSELKQEQKKVDELIAKLVKNR TRIVNESDVFVSWIRREFQELR HPVDEEKARCLEGIGGHTGLV ASLDMQLEQAQGTRERLAQAE LCWNSSEMRTTSSSSGSTPWP PVSRRRPWTERRLGVSVRGDLR ERSRPAVNRTPRMSRVPSGAPR GTPSRRWMMMKCWDHQMGR LVEEEVG

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14865	45233	A	14952	1	1513	MIILQKESLMSLQAQLDKALQ KEKHYLQTTITKEAYDALSRKS AACQDDLQALEKRTGRDWNW PPFRTQQRGSKSLTAIRPLCLFR KLNHVTSETKSLQQSLLTQTQEK KAQLEEEIIAYEERMKKLNTEL RKLRGFHQSELEVLIEEEMG NHNENTGEKLHLAQEQIALAG DKITSLERSLNYRDKYQSSLS NIELLECQVKMLQGLGGIMG QLSKTSSDSLKMK/RCY/TTW*M WTKLQFIHSILTSVIFHLLSFSSM GSI*KWIMALSGSSFLDAHYSIS QFGPRQLPSVCAEPEKEKATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQFAGQ*RHRL RGIMDEQWGYVGAKSRQRWLF YAYDSLRTTVVAHREQGSIK CKLEEDLQEQATKLEEDKREQLK KSKEHEKLMEGELEALRQEFK KKDKTLKENSRLKEENENLR AELQCCSTQLESSLNKYNTSSQ VIQDLNKSMPMEIRFQLYIFPDQ
14866	45234	A	14953	125	363	INVSVWSQPFPGG*QPEKGLKE HPADARPGSCPPAGRVPQGRA EVASAAAPRGSSPAAAPGQSH PSCLRAPLYWSFSR
14867	45235	A	14954	306	583	TCSTRRRKNDLSVKYVSVWSQ PFPGG*QPEKGLKEHPADARPG SCPPAGRVPQGRAEVASAAAP RGSSPAAAPGQSHPPSCLRAPL YWSFSS
14868	45236	A	14955	225	407	LRGMVTFSPFSSILNGQFENSG CPL/CPVCWVCLREPGDPEKLG EFLQKDNISVHYFCLVS
14869	45237	A	14956	484	722	NTCRCGHNRSPVNSRRGGLRS JPRMPDAGSCS/PPAGRPSAGPG RRSPPLLPRGSSPAAAPGQSH PSSSQGAIVLEL

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14870	45238	A	14957	434	1790	GNFFRKTIACIIISVLSYLVSCLR GASPTASMDFLKTSKREAR ASRKICFVCKKKGA AINCQKDQ CLRNHFLPCGQERGLPFTIFWR VQIIL*QTSP/EHRTSNMGHVGE ESCILCCEDLSPTCLRTFQSPC CSQAIYHRKCIQ/TNMPHQSK HFFKCPQCNNRKEFPQEM/REN GNSYSRQRCCLGTRARGFLRLI SALSAL*CPHLVCMNKAETALR MKGGGASFCVLHADPTEPTGT APLLDLTVRNGSVRSVHL/PA TDYIPENSGDIPCCSSTFHPEEHF CRDNTLEENPGLSWTDWPEPSL LEKPESSRGRRS/VLLEVQGCQ NH*QLQKIQVTPSE*LLVPHNR V*TCAPPSGLGREHSGTVRQGS RASSETMS/LSKEKSQWSMRRE QSRCCQGNAFMATRVPLLSPLL LPPRILPP*SCFHMPLLTSPMFV VMQIKVFSPPKKKK
14871	45239	A	14958	146	484	
14872	45240	A	14959	228	353	
14873	45241	A	14960	214	722	TARELPGRVLKEMYIQK*EGA ALGRPTRPGRQGQVRRAECR RLFRGVLRPCNRC
14874	45242	B	14961	1	951	
14875	45243	A	14962	241	517	QSCGQRLPTVLR/PLRTPWILPM YPQPLPAGGPTCLRSRPYINITI LKGDKGDPGPMGLPGYMGRE GPQGEPP*GSKGDKGEMGRP RRPVP
14876	45244	A	14963	748	1055	DRKQTSFGDAYHTIPGSLSSSD HVLSEPD*GEGSHL**SVQHD VPPTA**RLQYRAVVLFTATL PAILIM*GMRCLVPRNCSRTW TAQIRAYIEVQQT

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14877	45245	A	14964	1	832	MPHVCAQRRLPVAAVLPPDGA QNCILLAGLSAGTFCCHGGVHI LLSNPVATSLLV AIDRVGGIPIPP PPPPALPYDCCPPPSRHTEDRE HVPILPHWKLMVNRWFLPVPT EWIATLSNSSRSRTCMSQGLSF LDSQVHLKAMIEDLRGNVSKES SPCLADNADVGQFPMEGGQKD PKQRIIPFCQGVTNLSGPHGPGA VCGGSHYQKQESSEISLSVGGV WTSSRRMSQVGGSSHCRGARL GPCNVPRRPGVQDEFSLQPEE DAG*QTSVDPMLVEQYVVVA/ NYQKQESSEISLSVGGV/VVDIIE KNESGWVWFV/STAEQGWVPA TCLEQMGCRMSFLCSLKKML DWIQRVSL
14878	45246	A	14965	1	346	
14879	45247	A	14966	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDAIPLL
14880	45248	A	14967	1930	5781	RAKSPANIIMTGSNSHITLTN VNLNSPIKRIHLASWIKSQDP SVCCIQETHLMCRDTHRLKIG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFPSAPHHSYKIDHILGSEA LLSKCKRTEIITNYSLSHSAIKL ELRIKNLTQSR
14881	45249	A	14968	1	2235	
14882	45250	A	14969	1	2148	
14883	45251	A	14970	1	1821	
14884	45252	A	14971	1	1248	
14885	45253	B	14972	4	2121	
14886	45254	A	14973	1	1137	

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14887	45255	A	14974	1	1240	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGFNICKSI NVIQHINRAKDKNNHMSIDA AFDKIQQPFMLKTLNKLIGDGM YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLFSIVL EVLARAIRQEKEIKGIQLGKKE VKLSLFADDIMIVYLENPIVSAQ NLLKLSNFSKVSQYKINPVQKS QAFLYTNNRQTESQIMSELPFTI ASKRLKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMPFFTELEKTTLKFIWNE KRARIAKSIPSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEITPHIYNLYIF DKPEKNKQIQKAFILHAKEPWV MWNMGTNVR
14888	45256	A	14975	1	2241	
14889	45257	A	14976	1	2802	MYGTGYRDVAGKWAIDPDSK REFLDVTQEQIGGCDFSGTCRQ TSLILTOPLRQWGLEGIKKPN WIIEESVSNGGPPLIPRQTAS GVDLQQTPTDQLRLVTVRRK TNKQKGIASSTKRTSTPKPHL YVTIHKDSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWYVVRPDLRLIGVPD SDGENGTRLENTLQDI
14890	45258	A	14977	1	2739	
14891	45259	A	14978	1	2478	
14892	45260	A	14979	590	727	
14893	45261	A	14980	1	3255	
14894	45262	A	14981	1	3810	
14895	45263	B	14982	1	3127	
14896	45264	A	14983	1	3325	
14897	45265	B	14984	1	1734	

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14898	45266	A	14985	1	2067	MELKTKARELREECRLRSRCD QLEERVSADEMEDEMNMKREG KFKREKRIKRNEQSLQEIWDYVK RPNLHLIGVVPETDGENGTLEN TLQDIIQENFPNLRQANVQIQE IQRTTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTIR EYYKHLHANKLENLEFMDKFL DYYTLPRLNQEKVESLNRPTG AEIVAIIN/SLPTKSPGPDGFTA EFYQRGILPNSFYEAIIPLKLG RDTAKKENFRPISLMNIDAKILN KILAKRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHVNR KDKNHMIIISIDEEKAFDKIQPF MLKTLNKLGDGMYFIIIRAIYD KPTAHIIILNGKKLEAFPLKTGM RQGCPLSPLFNIVFKVLARAIR QEKEIKGILGKEEFKLSLFADD MIVYLENPVSAQNLLKLISNFS KVSQYKINVQKSQTFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPKVPMTFF TELEKTTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKATWYWYQNRDIDQWNRT EPSEITPHIYNLYIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLDPFLLPYTKINSRWKD
14899	45267	A	14986	1	1293	
14900	45268	A	14987	1	3229	
14901	45269	A	14988	1	3352	
14902	45270	A	14989	1	1419	

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14903	45271	A	14990	1	1716	MKA EIKMFFETNENKDDTTYQN LWDTFKAVCRGKFIALNAHNR KQERSKIDTLTSQLEKEKQEQ TYSKASRRQEITKIRAELEKET QKTLQKINESRSWFFERINKIDR PLARLIKKRQKNQMDTIKND KGDITDPTETITTVREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEVEESLNRPTGA EIVAIINS LPTKKSPGPDGFTA EFYQRYKE ELPGRDTTKEENFRPISLMNIDA KILNKILANQIQHIKKIHHDDQ VGFIPGMQGWFNIRKSNVQIHI NRAKDKNHMIMSIDA EKA FDKI QQPFMLKTLNKLVL EVLARAIR REKEIKGIQLGKEEVKLSLFAD HMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFRENYKPLLKEIK EDTNKWKNI PCSWVGRINIVKV AILPKVIYSFNAIPKIPMPFTEL EKTTLKFIWNQKRARIKSLISQ KNKAGAITLPDFKLYYKPTVTK TAWYSYQNRMDQWNRTEPSE ITPHIYNYLIF
14904	45272	A	14991	1	702	

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14905	45273	A	14992	473	2385	HSFLSFIVLMYLTMDLTRSQKH GWASSPSHGTSPWPVRLRTSLA KPKCKWQVSLCWVLSASPGSSF SLVRSLLIIVPHAESVSRRLPSLL SRVGLFPARY*HRVWQSRSPSQ TRDHLIKRNPQDV*RRQQPRG TRVSNKCSLHTSALGGRQPSC DATL*GQQGLP/VK*KRQQPAP/ MSQQQTGAALVLAIRAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPTVSAQNLLKLSNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRITYLGIQ LTRDAKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKEPGWARSLVFGARGLQG QGRCGQSRGGGSCGGGGST ENWQHREPSARKTGSTENRRH REPAAPRTGSTENQHREPAAPR TGTENRHREPSARKTGSTENRR HREPAAPRTGSTENQHREPAAP RTGSTENRHQEPAPRTGGTENR QHREPAAPRTGSTENRHREPAAP RTGSTENRHQEPAPRTGSTEN RQHRESAAPRTGSTENRHQEP APRTGSTENRHREPSAPRTVGTE NRRHRELVAAPRTGGTENPREP PAGTRPRHTPMRGGSEGALFH QRRFLEPTPDREQLEGIRYPPVA

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14906	45274	A	14993	687	2274	LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPVSAQNLLKLISNFSKV SGYKINAKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNI PCSWVGGRINIVKMAIL PKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARMASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNYLIFDKPDKNKQW GKDSL FNK GWENWLAICRKL KLDPLTPYTRINSRWIKDLNV RPKTIKLEENLDITIQDIGMGK DFMSKTPKAMATAKIDKWDL IKLKSFCIAKETTRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYA AKKHKRCSSSLAIRE IQIKTTMRHYLTPVRMAIHKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMRKNKTK TLI
14907	45275	A	14994	1	3189	
14908	45276	A	14995	1	3351	MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSAMEDEMNMK QEGKIKRKDEGHYIMVKGSIQQ EEL.TILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDYRTLHPKSIETYFFS APIIHTYSKIDHIVGS
14909	45277	A	14996	1	3192	
14910	45278	A	14997	1	2742	
14911	45279	B	14998	1	2313	
14912	45280	A	14999	1	1542	
14913	45281	A	15000	1	3300	
14914	45282	A	15001	1	1824	
14915	45283	A	15002	1	2982	

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14916	45284	A	15003	1	2375	MSGFLISPKHKHGTNSGIVSWA DVQSQLRHIEAFAFDQEA AAVL MARLGVFRAESEEQPDVLRWL DRQLIRLHSLTTLDIVPAGKGE VVKGPMSISQAKGCKFGQY NKEDPTSFRLSDFSLSYPQFMF HLRRSPFLQVFNNSPDESSYYR HHFARQDLTQSLIMIPIYSYS FHGPPPEVLDDSSILADRILLM DTFFQIVLYGETIAQWRKAGY QDMPEYENFKHLLQAPLDDAQ EILQARFPMPRYINTEHGGSQK KREKNQIDAINKDKGDITTEPTE IQTITREYYKHL YANKLESLEE MNKFLDTYTLPRLNQEEVESLN RQITGSEIEAIIINSLPTKKSPGPD RFTAKFYQRTNDQKHMISIDA EKAFDKIQPFMLKTLNKLGDID GTYFKIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSLLLF NIMLEVLAIRAIQKEIKGIQFG KEEVKLSLFADDMIVYLENPIV LAQNLLKLISNFSKVSQYKINV QKSQAFLYTSNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRF NAIPKLSMTFFTELEKTTLEFI WNQKRARITKSILSQKNKAEGI TLPDFKLQYKATVTKTAWYSY QNRDIDQWNRTEPSEIVPCIYN YLIFDKPDKNKKWGKDSL FNK
14917	45285	A	15004	1	1428	
14918	45286	A	15005	2	1975	

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14919	45287	A	15006	1	3891	MKPEIKMFFETNENKDDTYQNL WDTFKAVCRGKFIALNAHKKR QERSKINTLTSQFKELEKQEQT NSKASRRQETIKIRAELEKIEITQ KPLQKINESRSWFFKINKIDRP LARLIKKKREKNQIDAINKDKG DITTDPTETIQTIREYYKHLN KLENLEEMDKFLDMYTLPLN QEEVESLNRPTGSEIAHNSLP TKKSPGPDGFTAEFYQRYKEEL VSFLKLFLQSIKKEGILLNLFYE DSIILKPKPGRDITKKENFRPISL MNIDAKILIKILANRIQQHIKKLI HHQVGFIPGMQGWFNIRKSN VIQHINRTKDKNHMIIISDAEKA FDKIQQPFMLKTLNKLGIHGT LKIIIRIYDKPTANILNGQKLK AFPLKTGTRQGCPLSPLVFNIVL EVLAWAIRQEKEIKGILGKEE VKLSLFADDMTVYLENPIISAQ NLLKLISNFSK VSGYKINVQKS QAFLYTNNGQTESLIMSELPFTI ASKRIKYLGLQLTRDVKDLFKE NYKPLLNEIKEDITNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTDLEKTLNFIWNQ KRARITKSILSQKNKAGGITLPD FKLYYTATVTKTAWYWYQNS MVLVVPKQRYRSEQNRLRN NAACLQLSDL
14920	45288	A	15007	1	4215	MHSCLPDATGEGELYNSLGLST WSFLSMIGVLLWVDFSGDSIDL CSPLWNRTNLEALQKKLEEL DEQQRKRLEAFLTQKQKVGEL KDDDFEKISELGAGNGGVVFK VSHKPSGLVMAKLIHLEIKPAI RNQIIRELQVLHECNSPYIVGFY GAFYSDEISICMEHMLVQLQER PCPGFLWMENSDYGLLLPLDLL LCLSFSSKVLSDLVSDLIHGM KARNRSIHGDVVVVELLPKNE WKGRVTALCENDC
14921	45289	A	15008	1	2823	

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14922	45290	A	15009	1	3253	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKWKRTEITNYSLSH SAIKLELRIRKNTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRQKERSKIDTL TSQLEKEKQEQTHSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNK
14923	45291	A	15010	1	2816	MEDEMNMKREGKFKREKRIK NEQSLQEIWDYVVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIEIQRTPQYRS SRRATPRHIIVRFTKVEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFFTCICDDAEDLQSPSTA GPWFGVLYTKGGPYQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPQCH IGEVLDDGFTAEFYRRYKEELV PFLKLQFSIEKEG
14924	45292	A	15011	1	3347	MGDFNIPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTEYTFSSAPHHTYSKIDHILG SKALLSKCKRTEITNYSLSHSA IKLELRIRKNTQNCSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRQKERSKIDTLT SQLKELEKQEQTHSKASRRQE TKIRAELEKETQKTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDAIKNDK
14925	45293	A	15012	1	3855	MGGKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRSSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLSR CDQLEERVSADEMNMKRE GKFKREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL
14926	45294	A	15013	1	2559	
14927	45295	A	15014	1	2956	

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14928	45296	A	15015	1	1853	MGRNQSRKAENSKNQSSAPP KDCSSSPAMEQSWTENDFDELT EVGFRRSVITNFSELKEHVETNL KEAKHLEKRLDKWLTRIKSVE KILNDLMELKTMAQELHDTCTCR SFNSQFNQVEERVSVIDQINE MNIDGTYLKIIRAIYDKIPPRNII LNQOKLEAFPLKTGTGRQCPLS PLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNRRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIASILSQKNKS GGITLPDFKLYYKATVTKTA/W L/YHTPLSCLPP*WNRTEPSEIIP HIMAVAQIQQVKLLLLQGQHA SSRLQPTSSTKCGGWTAASSAP RSMGLSSWKGNLASAIHYFPCK PLTLPSRISTSSSSWGCRQAHAV LEVLRWPPGLGWPGWIIHLTL HVPPVRITKSNGPRACTRASAS HARHHQYNQFPLSPLHSPLPP PEQVLVSTAERTEDRSYHRTL RHSPYFKNEAADLRGEGYSS
14929	45297	B	15016	1	3276	
14930	45298	A	15017	1	2274	
14931	45299	B	15018	440	3383	
14932	45300	A	15019	1	2646	

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14933	45301	A	15020	1	2229	MGKKQNRKTGNSKTQASAPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRLSR CDQLEERSAMEDEMNMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLRQANVQI QEIQRTPQRYSSRRATPRHIIV FTKVEMKEKMLRAAREKEIQ TIREYYKHLVANKLENLEEMD TFLDTYTLPRNLQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGT AEFYQRYKEELVPFLKLFQSI KEGILPNSFYEAIIIPKPGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVQHINRAKD KNHMIISIDAFAFKIQPFML KTLNKLIGIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTQR GCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLIISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKIGKTTLKFIWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWYWYQNRDIDQWNR
14934	45302	A	15021	1	960	
14935	45303	A	15022	1	2928	MEDEMNMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLRQANVQIQEIQRMPQRY SSRRATPRHIIVRFTKVEMKEKM LRAAREKDRSMRQKVNKDQTE LNSALHQADLIDYRTLHPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEITNYLSDHSAIKLE LRKLNLTQNRSTTWKLNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDAP
14936	45304	A	15023	1	1782	
14937	45305	A	15024	1	4881	
14938	45306	B	15025	1	5962	

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14939	45307	A	15026	1	2053	MKAIEIKMFFETNKNKDDTTYQN LWDAFKAVCRGKFIALNAHKKR KQERSKIDLTLSQLKELEKQE THSKASRRQEITKIRAELEKEIET QKTLQKINESRSWFERINKIDR PLARLLKKKREKNQIDAINKDK GDITTDPTIEQTITIREYYKHLYA NKLLENLEEMDKFLDTYTLPRLN QEEVESLNRPIITGAETVAIINSLP TKKSPGPDGFTAELYQRYKEG AVLEVLAIRQEKEIKGIQLG KEEVKLSLFGDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYGF NAIPKLPMTFFTELEK/TT*KFI WNQKRARIK*ILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWSRTEPSEIMPHIY NYLIFDKPDKNKKWGKDSLNF KWCRENWLAICRKLKLDPLFT YTKINSRWIKDLNVRPKTITITLE EKLSTNIQDIGMGKDSMSKTPK AMATNVKIQKWDLIKLSFCT AKETTIRVNRQPTTWEKIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKVVKDMNRHFSKEDIYA AKKHKMKCPSLAIREMQIKTT MRYHLTPVRMAIIKSGNNRC
14940	45308	A	15027	3	3229	
14941	45309	A	15028	1	3907	MGDFNTPLSTLDRATRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFPSAPHHTYSKIDHIL GSKALLSKCKRTEITNYLSDHS AIKLELRKLNLTQNRSTWKLNS LLNDYWVHNEMKADIKMFFE TNENKDDTTYQNLWDTFKAVCR GKFLALNAHKKKQERSKIDTLT SQLKELEKQE/THSKASRRQE TKIGAELKEIETQKTLQKINESR SWFFERINKIDKPLARLIKKKRE KNQIDAINKDK
14942	45310	A	15029	1	4005	
14943	45311	A	15030	287	2708	
14944	45312	A	15031	1	4602	
14945	45313	A	15032	1	4806	

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14946	45314	A	15033	965	5928	TWKGTTSTRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRKLNQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQKLEKQEQTHSKA SRRQEITKIRAELEKEIETQKTLQ KINESRSWFFERINKIDRPLRLI KKKREENQID
14947	45315	A	15034	383	8708	
14948	45316	A	15035	2	3257	WRKIYQANGKQKKAGVAILV/S DKTDFKPTKIRDKEGHYIMVK GSIQQUELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLSTLDRLMRQKVNKDTQEL NSALHQVLDLIDYRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRKLNLTQSRSTTWKLNNLLN DYVWHNEMKAIEKMFFETNEN KDTTYQNLWDAFKAVCRGKFI ALNAYKRRKQERS
14949	45317	A	15036	1	3508	MELKTKARELREECRSLRSPCN QLEERVSAMEDEMNMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTLEN TLQDIQENFPNLAQANQIQEI QRTQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSHSAIKLELRKLNLTQNHST TWKLNSLLNDYVWHNEMKA EIKMFFETNENKDTTYQNLWD TFKAVCRGKFIALN
14950	45318	B	15037	1	4760	
14951	45319	A	15038	1	3110	
14952	45320	A	15039	1	5546	MELKTKARELREECRSLRSTRN QLEERVSAMEDEMNMKREG KFREKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDAENGTKLEN TLQDIQEDFPNLAQANVQIQE IQRTQRYSSRRATPRHIIVRFTK VEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQUEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE

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14953	45321	B	15040	1	4534	
14954	45322	B	15041	1	1826	
14955	45323	B	15042	1	1626	
14956	45324	A	15043	248	1212	NSKHYSRGQKKKLPTLPRAAN SRWRSLLK/GFTVSFDETLKPFV RDVSGSRLKDLPKPNKSDDETR ANDAVNRYKLLKKDARTIAAQ QVARLESAMCLRRRWLENFQ LFLVEHPLVRHLTRRLIWGVYS AENQLLACFRVAEDNSSSTADD DLFTLPEGDISIETHVLEISPTD AAALLFADYELLPPFRQLDRNS YALTEAERNASELTRWAGRKC PSGRVMGLANKGWIKGEPQDG GWIGWMIKPLGRWSLIMEIDEG FAVGMSPAELSAEQLLSKLWL WEGKAERYGWSNSTQEAQFS VIDAITASELINDIEALFE
14957	45325	A	15044	1	1788	
14958	45326	A	15045	1	3048	
14959	45327	A	15046	1	3546	
14960	45328	A	15047	969	1205	SPVRCCISAVHRTYHRRTSALL RLAELHRLLEKCSARQWMYEN I*SPFRQIA*CLPYS DHKNQRLH GLDSIFLARLLW
14961	45329	A	15048	877	1248	WPLTVPYCGVGYAS*A*VADN HRAVGYLSRWAGRKCPSGRV MG/LANKGWIKGEPQDGGWI/G WMIKPLGRWSLIMEI/DEGFAV GMSPAELSAEQ/LLSKLWLWEG KAERYG/WGSNSTQEAQFSVID
14962	45330	A	15049	854	1313	DHGVASAAATCVYTNHGRQSY VRVCEYASRTRVSHHCSV*RVL RCEAIRIVSPDRSC*RDPEFSYL ALPENYNRLFLPNSTNQTNRI KTLNSIAIGKLLAAGGVYNGNI EGFRDTAEKLDGRTIDGYDQIL NEKTAVIAKATA/SILLTKRS
14963	45331	A	15050	1010	1396	KPFGKLYTKLFEGHAWLVKAE KVRVGYYRLRLTYPFDIRFPAL PFGLVL*KGAHFTVPRIWAGHA C*LMPMALPMFRWKVTGLLFIP ICLVKPSFLTLTHIAIRRISTSN CRKTPKQPSRWCKPR

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14964	45332	A	15051	361	837	DGQQLIALHRLALREIQQAVH AGLPQQAQKILFDGGSEIGKIPSEI YFCQLVKLILCPVLFPWCRRVA ILWRRRDVLFSGSFSALVSPH LCG/SYLPFVFDVGDRL*LSVG WSKEIWPCK*GFGHLMVSLNT PMKSLVEGFKHFPLAGFGYEYL SFFCR
14965	45333	A	15052	1563	1652	
14966	45334	A	15053	2756	2995	AMRSAHRCVTFSAALLNCWQITP HLTPSVMICGQLLTLVNRCPSS TIFSIPLSKQVARMFRSAMSPL NRARCWKVPCN
14967	45335	A	15054	762	2184	WRAPSEPISEILKADTEKYVY L*NSSSAQYSGSCTRAYYLDLTDQ HPTPRLCLIFGGKDSGLMLHLT AELARQMGKKICVLFIDWEAQ FSCTINYVQSLRELYTDVIEEFY WDALPLTTQNSLSQYQPEWQC WEPDVEWVRQPPQDAITDPDF CFYQPGMTFEQFVREFAEWFSQ KRPAAMMIGIRADESYNRFVAI ASLNKQRFADDKPWTTAAPGG HSWYIPIYDWKVADIWTWYA NHQSLCNLYNLMYQAGVPLR HMRICEPFGPEQRQGLWLYHVI EPDRWAAIGSPADREDAEEYL EAIMEARVTVAGMGLVMEVQ DYFDGEADRLAKAWLAEYTPQ IKSLKDERKEAYRQIVEMSTEP QDVDLVRPANKFEMTRVREG KEADLPVWKHLLCDESGNYP ALLNHWETKVFEIETKREGFAF WYRNPOYTQSSSLGIAYVEAE QYKIVRPDLFFAEQDGKMOVV
14968	45336	A	15055	2069	2586	PWLENLPVGCWSAVKMGGT RSLVSL/AVTLVSPQLMAYL LGQQLPEVWDFGMFSIAKVG YQAQVIALYLVVVVPCSLILAV FLAHALIGPFRMIGDGVAFV RHLMTGSFAPIGAALFGFLYAP LVITGVHQTTLAIDLQMIQSIGC TPVLPVNALSIDLWHISILV

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14969	45337	A	15056	356	1205	APASMTFEQVRFVA/VMVFTK RPAAMMIGIRADESYTVLSPSP V*INNVLPTITWTFPQTIYDFLW LIGEAIF/YLPVGICWSAVKKM GGTRSLVSL/AVTLVSPQ/MN AYLLGQQLPEVWDFG/VCSLIL/ AVFLAHLALIGPFGRM/GDGVA FAVRHLMTGSA/PIGAALFGFL YAPLVIT/GVHQTTLAIDLMM QSMGGTPVPWPLIALSNIAQGS VIGIISSRKHNREIPGEVFPRT GVGKGLSLG*PLH*LQPYRQHL GAGSYSQTLKKQIAESAVRLSIP
14970	45338	B	15057	1	435	
14971	45339	A	15058	2	1785	WLLYRAHVKG/STEALLPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLLGDKVIPATIL GIQSDRVIRGHRFMGEPTIDN ADQYPEILRDSGKVIADYEERK AKIKADAEAAARKIGGNADLSE TLLEEVASLVWPVVL/TAKF/E EKF/LAISRTALVPYASADNMYQ LVNDVQSYPPQLPGCTGSRILES TPGQMTAAVDVSKAGISKFTTT RNQLTSNQSLMNLVDGPFKKL IGGWKFPLPSQEAACRIEFHLD FTNKLIELAFGRVFKELAAANMV QAFTVRAKEVYSASMRYYIVIV YISYRPPNLLDSHIGFSSITTHC AVTSHHYNSCDMTMTIHSYVT PYISVRVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDTRHIHTI ESRCRVCGAHDSDAERLDRF AQTADRIADRGFSSRPECIRS LAFGEADYIVRVHWRGLRWLT AEGMRDFMMGFLRGLDCALIS KTRLLSENRRKGRVVQAETLE AAGHVLLLTSLPEDEYSAEQVA DCYRLRWQIELAFKRLKSLHL DALRAKEPELAKVGIFANLLAA FLIDDIIQPSLDFPPRSAGSEKKN
14972	45340	A	15059	1	993	

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14973	45341	A	15060	1	5621	MSEKTLFLVEIGTEELPPKALRSL AESFAANFTAELDNAGLAHGT VQWFAAPRRLALKVANLAEAG PDREIEKRGPAIAQAFDAEGKPS KAAEGWARGCGITVDQAERLT TDKGEWLLYRAHVKGIEGTEA LLPNMVASSVAKLPIPKLMRW GASDVHFVRPVHTVTLLGDK VIPATILGIQSDRVIRGHRFMGE PEFTIDNADQYPEILRERGKVIA DYEERKAKIKADAEAAARKIGA KAWGTNVEFHVQNPQ
14974	45342	A	15061	82	732	
14975	45343	A	15062	1	3849	MDLGANGWQTFRYVVLPLNLS ALLAGMGLAFALSFDEIIVTTFT AEQVDAAVRAADAFAEWGQ TTPKVRAECLLKADVIEENGQ VFAELESSNNTAFARASSNGDL PTKADLQAQLDSLKNQKDLA QDKLVQQDLTDTLATLKDIDRI KEETVQLRQKVAAPEKMRQA TAALTALSDVDNDEETRKLST LSLRQLETRVAQALDDLQNAQ NDLASYNLSVLSTQTPERVQ NAMYNASQQQLQIRSRDLG
14976	45344	A	15063	219	1186	PPKLGKRKGIFLPSHSNPNTNRI CPNCCMNGVSTANTTSKSSLVI CAWTKHALLNAILQPEQLWKS GSRWRINLALPRGYRESLLQPW QAERLTDDKGEWLLY/RAHVK GESTEALLPNMV/ATSLAKLPI KLMRWG/ASDVHFVRPVHTVT LL/LGDKVIPATILGIQSDRVIAA TGKAKIKADAEAAAR/KIGGNA DLSESLLEEV/ASLVEVPVVLN AKFDEK/FLAVPAEALVYTMKG DQ/KYFPVYANDGK/LLPNFI/ VANIESKDPQ/QIISGNEKSFVR LADAEFF/NTT*KRLFLPHQKL PPSQILHQQTRNYASFCHRRHD NWTSA

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14977	45345	A	15064	1	1496	SGGCAGLHGGILCSKEPFQASV QQGVAGHACAPAAALQVPVCGT LSDCGSRAASLCENPFSISLYGR LVATSLAKLPIPKLMRWGASD VHFVRPVHTVTLALGDKVIPAT ILGIQSDRVIRGHRFMGEPEFTI DNADQYPEILRERGVADYEE RKAKIKADAEAAARKIGGNAD AKFEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIFVA NIESKDPQI/DRIQALAGWIAE QNGADVNHATRAGLLSKCDLM TNMVFEFTDTQGVMMGHYAR HDGEAEDVAVALNEQYQPRFA GDDLPSNPVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRIIVEKNLNLDLQTLT EEAVRLYGDKLTANVVDVVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPTRPADFDWHALG RAGTGDVVVGVRGLAIVPLT DGLDEAGHSTGVLQGEVPQRL ERAFTVPGVTLQPQALQARGL
14978	45346	A	15065	134	384	VTPTGWRKRRIRQWCS DAGCG VNALSLGRFHSALFSAAMFI LGVVSGITMSISP*ILSCVRSKNP LLVSGSGPLSCNSTIH
14979	45347	A	15066	1	723	TKSPKIARSRHPLCHFIFERRPI MTNSNRKLTWISFLSYALTGA LVIVPGMV MENIADYFNL PVSS MSNTFTFLNAGILISIFLNAWLM EIVPLKTQLRFGFLMLVLPVAG LMFHSLSALFSAAMFILGVVSGI TMSIGTFLVTQMYEGRQGYR LFLAASLFSMAGMIFPMIAAFL LAPSS*W*WVYACGLAYVTIF IMTFGCEFPALGKHAPKSYAPV EKVKWGILGGASSFRAV
14980	45348	A	15067	422	1045	LLEGKLTNRKQ*HQH*QKARPC KKPIQSAQN/WNREEDDELTEV GRRVWIITNSFELKEHVL TQWK EAKNLDKRLQEGLTRITSLEKKI NDLMVLKNTARELHEAYTSINS RIDQAEERISEIEDQLNEIKLED KIRGKRJK/RQTNKQSL*KMWD YVKRPNRLIGVPESDEENVTE LENTLQDIHQENFPNLRQANIQ IQEIQTLLR
14981	45349	A	15068	1	1131	

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14982	45350	A	15069	383	756	LNPSNKLALINPAASPIIKGVDL TANQ/PCIAIDIPLYDADVQQE* CFPATVEALGEQIRQADGVVIV TPEYNYSVPGGLKNAIYWLRL RQILVFLDAMVMNKPPEFMGGV IQNKVDPQTGKVIDH
14983	45351	A	15070	343	924	
14984	45352	A	15071	223	308	
14985	45353	A	15072	57	5546	NKMARKKFGSLEISLIVLFVIVT IIAIALIVVLATKTPAVDEISDST STPATTRYTTNPSDSGKCPNVL NDPVNVRINCIPEQFPTEGICAQ RGCCWRPWNDSLIPWCFVDN HGYNVQDMITTSIGVEAKLNRI PSPITLFGNDINSVLFITQNTQPN RFRFKITDPNNRRYEVPHQYVK EFTGPTVSDTLVDVKVAQNPF IQVIRKSNKTLFDTSIGPLVYS DQYLQISARLPSDIYIGIGEVH KRFRHDL
14986	45354	C	15073	1	1818	
14987	45355	A	15074	493	576	
14988	45356	A	15075	381	498	
14989	45357	A	15076	48	514	LLLFLLLQSYDWSSESGKRQSAL HGRQKGLPKSPTAARGGSDPW PSCRHP*GPNRKRKRS/R*PMET APRRPSVSPALTPARPPGLTATP RLHPRPP/RSPNPSANLLRRPTP DT*AHATFGPGRSRHHFPGQLS TE/RRRSAEGGRSRNEASRRE GGE
14990	45358	B	15077	1	1116	
14991	45359	C	15078	249	332	
14992	45360	A	15079	710	1326	RAAGNCFPEPGFVKQLSAAAA VVAPAAAAEGSIPDTGKSPSSI SHWPNPQKNVICKRRGRVEQE QAWKGR*RVVFLG*KSMRCP VDLLPQSCLCQRFHQ/GKWIL TKDYIIHSAKSGRWLDATTYE WGYKIEKDSRYSPQMQSAPKR WREELKRTGAPGAFHRWKVVL LVRTDKRSDSLRFSDNFGDCDI RMEKTFRTLMES

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14993	45361	A	15080	602	1257	FGKRGRTITLCILAVGMLCCRK GHTKPRRRPGASPISTHLHSSPPI STHLHTSPPPHREEAR\SGQ*R QSCGAAAR*PWW\NCDGWG PKCQRFKSH*DIAQPDEVSWGQ *PWAVGALAGPIH/PQASEGPL GCTPASICGSTRKPSKPLSKKPP QAARTSSSRIVIFTPISTRPPTQG QPEKAKSATPTNDLEGPSAKVK FVNFLMDETFPEPSFFI
14994	45362	C	15081	140	175	
14995	45363	A	15082	2295	3089	NLLGYQINPPLQIFWDKLLAV SERDSSVKEESGDVESDDTML* MLPCP*ETTEFSS*PFRJSS*LSS* STAQIPAECTCFAGGWYSIFCPQ RIEQETMCLL*SWQSEVAVSCE SPWPTALHHSHPNRAPPPCY/S KSTSSSLSPLENSG*QNRPPSLL ITSVLPLRITCLP*VSFIPPIMQLG GSFLSNDRL*QSFLPKNVSLF VSFPLI*GAVSKPAISFNTSVSPL LVSDIFFALSLLP*GLGTWLIPSS SLLLVVRF
14996	45364	B	15083	143	1727	
14997	45365	B	15084	307	1017	
14998	45366	A	15085	1	959	MSRMGLLGFGERKELPNHPAV SEWPLTLVTGSSGTVAEGEGN LTTSGLFSIVLHPDGVAAQGR HSSLPRWGSQAEALLTSQTVDG QAEMLLTPQTMGGQEEMLLTS QTTGEDFITRSTESGTHSKSHKG DEGEPRWMLGWMLWVCDIAE PLVKAKLLDCKHTCCSVCLQQ TRTSQKDVRCWPWCSGVTKLPD FSVSQLLDDPEVLAVITIPHASE HMPVFIRLPGSGCY\SCPCPSPRS TRCCPEI*AATCCPGTGRSPSL/C DHPCWTAASARQGSPPGGGGG AGQAGHGKLVVVEGVHCHL GGLRLGLPPQHRAP
14999	45367	B	15086	112	672	
15000	45368	A	15087	2	530	SGRSAALLSARVNRSSQSFAGVL GSHERGPRSPFVSPGPPRKP ALSRVSRMFSVAHPAAKVPQPE RLDLVYTALKRGPDGLLGAVH QQEQEKLQGIRESKRNS/RLG EWREGFLYDLDKQVKSIEFRL RLEFHASKIDELYE\AYCVQRR LR\DGALHMGRA\YTTGSPGSR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
15001	45369	A	15088	216	1369	EPVLRRRRPRQPRAGAQQGFPVFS PPGPPRKPALSRVSRMFVSAH PAAKVPQPERLDLVYTALKRG L/QAYLEVHQEQ/DKLQGOIR ESKRNSRLVMAGGVLTWTVV*E RGAVTSLASAGVLLIPPKYLPL LPTPAGLALYDLQKQKSIERFL/ RRLEFHASKVRVQHVCRWD/D ELYEAYCVQRRLRDGAYNMV RAYTTGSPGSRARDSLAEATR GHREYTE/DEGWGPMRQHRHS MCLLES/ELEAQLGEFHLRMKG CAVDINDLGTIKLSLEVTGAAS SVNKASTVTKRSPPIARAHRT PHFGNSFLSTRKPNTYTANHRR RPIEQHPDMRTPPPPHRARTNT GRKDKVRAHEGEKATPTTRTG APHGKAQRLRLPLYQYVTIATLS
15002	45370	A	15089	1	940	MSYNSKNYVETITTTMNSVKFG ETTPRNRTHYLSTNEKIFLSGV FSNAYPAGLSRGWDSPPWGSTP WVRHFCYLSSTQLCDQNCSSL SLLPAGPSVCNRLLASAWQKSS SSASSEASETCQSVSECSPTSD WSKVGSHEQPSGATLQRRKDR VE/PCETQSPGPASGGTLGPSGE EAPRPRMSPATIAAKHGEVSP AASDLAMVLTIRGMSL*HQKSS RDSLQYSSGYSTQTTTPSCSED TIPSQGRPAGLGPTKPVSIESTYL QSPQRLKQEWATEGKIQLPPQ IQVNVNQVDSSPSLPLIMVPEH MHVS
15003	45371	B	15090	1	777	
15004	45372	A	15091	26	336	KISPMINVCSESSPSGERRGA* TPPSPQSPGPKPSS/PPSCSPSR NYFLLFQGLCAEHPALAAPAAS VGTCPSPASGTHAAAPSGPWGR RCVHSGPGGRLW
15005	45373	C	15092	46	423	
15006	45374	A	15093	1773	2219	ELDYLYCSNNSAQCQPALLPSL ALPGPAGSARQAQSPARRLCAP VQPSGRWPAPGGPGFPGSSCPA SPTRQ*LLTSGSGCPRPCHHPFG PPQ*QSTQAWDWVILGPAHAG PSGQRCERCLPSRSGPQTHSG VGSEPRAVRGPVSVFV
15007	45375	B	15094	1	7916	

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15008	45376	A	15095	16	545	GLPWQRHVRVEECGRS/PLRPC SPGTPSPS*PLPAATRGPATCQS LSGLQPEKTT/SPS/CAAVAHER PPGPVPQCPAQGTGLIF*EGWT QPQIQRGPHPAHE/CAHDLQ QAAPGPGGAHQG/PSQPG*PDR QPDRAERAVVHPGAQ*DAEIQPG LPGEGGPLATRTERSPAQRPS QARG
15009	45377	A	15096	320	1167	MDLKTAVFNPARDGKLRLLTK *WASKSKEEVSSISEKTNGAT PLLMAARYGHLDMEVFLLEQC SASIEVGGSVNFDGETIEGAPPL WAASAAGHLKVVQSLNHHGAS VNNTLTNTSTPLRAACFDGHLE IVKYLVEHKADLEVSNRHGHT CLMISCYKKGHEIAQYLLVKG ADVNRSKSVKGNALHDCAESG SLDIMKMLLMYCAKMEKDG GMTPLLSASVTGHTNIVDFLTH HAQTSKTERINALELLGATLFT QKEISCDSESGRTRDLSPPRKPPH
15010	45378	A	15097	187	623	KLKTKNNIGPOACNSQLASVS TRSPPTLSVPIIMTDDSQASQL LLAAVTIRKLWSRMAPMLALP TGQSGQTGAEGQGKEGERGQS PCWKPRLDPKLC/EPQPAQLL* ADVCTGP/CGVRGCPADCRLLP LSPSSAQPKAESRSA
15011	45379	A	15098	789	1041	
15012	45380	A	15099	707	1373	SAWPSCHCHLDILSR/PGDDA CSVQILVPGLKGDAEGKDGK APGRPGRVPGTGEKGEKGDG DIGPPGPNGEPLPCECSQLRK AIGEMDNQVSQLTSELKFIKNA VAGVRETESKIYLLVKEEKPYA DPPLSWQGRGGTSLMAQDEAV HGLKGAYLQARLGRGFIGIHR PWKRRAPLLLF*TLSPRSF*KG DGGGNTQKGRKKRELAGQIW GPCIRR
15013	45381	A	15100	79	420	WRRFLFLGLVFRGYLGCLRSRS VLGRLKVSMDRIFFACGCGHL STLPSWPLRPSLWRL*EEQELP SLSVSPSSGRSASRL*LGWRGF GPSPSRLTVQFSGGRRAGQPS
15014	45382	A	15101	3	284	
15015	45383	C	15102	83	112	

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15016	45384	A	15103	84	303	EEQELPSLSVPSCLWGPCPRAG WLHSLHWPVSHSFSASTTFGM AIWT*SLASGIKPSQSSKVSRRQ VPPTM
15017	45385	B	15104	112	462	
15018	45386	A	15105	326	1323	DRKAINLQVKLEGAVAL*KPVG EAQLEFGKALGLFQ/STLGHFF VNNKEKILGDF/QEATLQAATK LTRGRSLVMENMEQLLSMRME DQSQRNMPLSVVLIREKAHSPF ENRKQEQGEGASPENFRAR/QG *FLAFKAAPPA*AASGPAAQER SVQEPSVNAPG*IPEGGLHTLA GVHHE*ALAWCSPLNKPRLW KRLP/SRTFHFPPVEDESAAGSKP SGDLLTLLGGNAAGDFKLK/P CLVYPSENPCFLKGSFKPNLPL VWCSSHKKA/WVQPG*QSETPFQ KKKKKKKKA/WVTMSLFQEW LHFCSTVE/ARCTQYDLQYKGL PILDSTPGHPCG
15019	45387	A	15106	3	375	HASAHASGLQSSYQAVKESS EALFEMKRDLTFTQVVOHDT ACTIAATASVVEKELATEGSSG ATEKMKKGLSDFLGVISDTFAP SPDKT/STAMSSPYDGTKARLY SLQSDPATYCNEDPGPP
15020	45388	A	15107	184	377	YCTNNQKVN*KTEIITKRKTPSR QKKDASAFSPSHPLTEGLK/WND LTLVSLSLTHDGFVWRRGKGV
15021	45389	A	15108	3	816	SWEDVGWWRSLWQQSYQAVK EKSSSEALEFMKRDLTFTQVVO HDTACTIAATASVVEKELAI CSRGAFLCPFSIQTEGSSGATE KMKKGLSDFLGVISDTFAPSPD KTIDCDVITLMTGPSGAEPYD GTKARLYSLQSDPATYCNEDPG PPELFDAWLSQFCLEKKGEISE LLVGSPSIRALYTKMPAAVSH SE/TFWHR/YFYKVHOLEQEQA RRDALKQRA/VSGDSCT*SGVL TNE*KGSWVRDTERVRSLLPQT FSEGVGWREC
15022	45390	A	15109	1	281	

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15023	45391	A	15110	1	1194	MGFLHLGQAGLEFLTSGSSDTI SEDWEKDFDLDMTEEEVQMAL SKVDASGEPPFCWKGYPGGEL ETLIRLLQKLFFLKTDPAFVLSP STLVKLHLWGNEGLQESLESV LHDAALVILVPNLEKKGEISELL VGSPSIRALYTKMVPAAVSHSE FWHRYFYKVHQLQEQAARRIA RLKQRAEQSISEEPGWEEEEEE LMGISPISPEAKVPVAKISTFPE GRTLAPQSPCEENLVTSVEPPA EVTPESESESIKSPPLTRALGTD
15024	45392	A	15111	213	1031	AGNKPDPWAGNRNRTAVLPDVS VFHREDVGVWRSWLQQSYQA VKEKSSALEFMKRDLTFTQV VQHDTVCTIAATASVVKELA TEGSSGATEMKKGLSDFLGV SDTFAPSPDKTI*RDVITLMGTP SGTAEPYDGTAKARLYSLQADP ATLLY*PDGPPFLFDAWLSQFC LEEKKEISELLVGSPSIRALYT KMVPAAVSHSEFWHRYFYKVH QLEQEQA*RDALKQRAEQSIFE EPGWEEEEELMGILPIFPKEAK FPLAKISYIP
15025	45393	C	15112	414	557	
15026	45394	A	15113	98	467	
15027	45395	A	15114	1	155	
15028	45396	A	15115	16	94	RCPIASEASWTITD*RCPIASEAS WTITDALGNSYSGGMAF
15029	45397	A	15116	95	115	IIRHLCND*TPREGCLSP*PAW SDTFETWVNNQASLQ
15030	45398	A	15117	3	282	LKPVITCLLQLGLLKPINSPYNS PTLPVQKPDPRYSKPNSLP*LNP SLLQRNYTSIFLLTNMPSISCT TMLLYGQKEISSLHKGPPSLMP
15031	45399	A	15118	548	1401	SCTPCWHLTGRLWGITA VRQK RHVLSVDPKLRHQSRGTGKAAPF WCLIIAGTPL*LYTHVSRVSDH AGMPALVHLPLQQVPLFWGRG NTL*KD*SLLSLAC/VQHGLLKP INSPYNSPILPVVVKPDKPYKLQV NLRLINQIVLPIHPVGEAPVPLE TGGKSGKDCILWFECHLSHNTI EHQVSSSTFRIVVATGVLVSLH PQLYMAQNREHAECLEGESKG REQESLSGNPENSRSLLTSRRY LYKSTRTIVLLGLAGPLKQKKL RSQHPSLYKYLQSRNKDSYR

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15032	45400	A	15119	144	298	WQVPLFWQPFPEPELWPKA/HLTDSFPDLLGLAAED*RCPIASEAPCTQVI
15033	45401	A	15120	449	667	
15034	45402	A	15121	2	111	
15035	45403	A	15122	323	401	LLGLAAED*RCWIASEAL*TITDAK
15036	45404	A	15123	2	593	CTLPSH*NLITLTPLNANIPSHGML*KD*SLLSLACYSTAF*GL*TPLTIPPFYLFKNQTRLTG*FRICPLSTKFLCSTPWCQTHILSY PQYLPPQPIFLFWISNMLSLFLCTL YPSLSSLSLGLTLTPIRLSKLP GPYCRKPSQTAPTSNHPSSFSGSWYSVETSYPSSSIFRKGRDTSWSLKDTPHQAQPPT
15037	45405	A	15124	354	630	
15038	45406	A	15125	29	354	RFLVSLMLPPAVVMLNHCYSLI FTNALVKRLFAWNMLSELATCAGNLATGPRNARSPGFLSCVP SVRDPTGNQT VQLTWQPLPEPL ELWPKA/HLTDSFPDLLGLAAE
15039	45407	C	15126	1	576	
15040	45408	A	15127	377	624	RDQLQCLQLWDAGACYTCWK SATGPRNAHSTVFLLSHVPSVW DPTENRTVHLTWQPLPEPELW PKA/HLTDSFPDLLGLAAED
15041	45409	C	15128	1	462	
15042	45410	A	15129	44	340	PCQTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHP*RQVPLF WGRGNHISGTQELPNT**TAV/V QAF/LPEPPPTG/CLLHVPEIWPL GQGM PAGQDSS
15043	45411	A	15130	242	522	RLVWPATQRAW SQSEAAAAK TVDLALSARN SATGPRNACSPG FLLSCAPSVWDF TGNRTVQLTR QPLPEPELWPKA/HLTDSFPDL LGLVTED
15044	45412	B	15131	1	1080	
15045	45413	A	15132	1	642	

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15046	45414	A	15133	245	1033	TALLLTQSLFGGLFTQTRMKFG AVTRIGGPPLGDQSPVLLFFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPI/ ASHSML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRFTG* FRICALSTKLFCCLSTPWCQTHIL SYPQYLPQSIILFWISNVLSSLF LCTLHPSLSSSLGLTLTPFRLS KLPGLYCRKASQTAPITSVKPK FLPYLLPISA
15047	45415	B	15134	146	556	
15048	45416	A	15135	1	555	LTSFLHCLLSHHYHGAQIHPRH FLHLICRCHCHQYCHHAYLDPC PQDSHHHLHWCWQPLPEPELELRP KA/HLTDSFPDLLGLAAED*HCP IASEAALPPCFPRPDMITSRLQL QRRRQTALGVRYRNATYRTRT ASTNSLRPRGSPFPLALVTNDR QVRSQALALWKRDRLLQLSPINR AISESSFT
15049	45417	B	15136	1	555	
15050	45418	B	15137	499	769	
15051	45419	A	15138	752	1111	MQPTIGNSQSVSRPTA*MPLAE SHPITQLVGTVTTPRVTPLSIRH PWRCRSANAGAMILTMKQLAI VMRVYQHQRVRRMRPGRNGA RSGMSAVGAYYSSCIRVM TAL QSCTGDDEAVLL
15052	45420	C	15139	1	632	
15053	45421	A	15140	1	375	PGVRGAQGGPSIPRQCEESAIGP KFAWIISSFFHWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGFIWQPLPEPELELPKA/HLTD SFPDLLGLAAED*HCP IASEAPA LVYTAGLHCFKPSQ

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15054	45422	A	15141	1	1340	CSEYEDSSPAPVPATDLSSTLSS SVPQPDGTGTSQQHLPLDPWHE LLRAQELQGATNHKGYSAAEH EHAGLG VQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSAFAFG LLNLHQWVFSGFQAFSDRLKA ALSASLLRFGSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTL QKRKKGMPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTDQPKHLTNFKSKTKET GFIHGPKTAPVTDWEGSLPLV FNHSGTPL*LFTHVSRVSDHAG MPALVLHP*RVQVPLFWRGKI* LTSPSRCTIIEKSCNSLPPL*DKP QPHLQHTRTSKCLNRSGQAF/L PEPPPTG/CLLHVPEIWPLGQGM PAARDSS

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15055	45423	A	15142	2	2107	IDMIFTPGPPSTPKHKKSQKGS AFTFPSQQSPRNEPYVARPSTSEI EDQSMMGKFVKVERQVQDMG KKLDFLVDMMHQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSCLKTIICNYSETGPPEPPYSF HQVTIDKVSYPYGFHDPVNL RGGPSSGKVQATPPSSATTYVE RPTVLPLILLDSRVSCSHQADL QGPYSDRISPRQRSITRSDTP LSLMSVNHEELERSPGFSISQD RDDYVFGPNGSSWMREKRYL AEGETDTDTPFTPSGSMPLSST GDGISDSTVPLFLSSEILKQVVG QSITSMGLGFLSRGSPMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFSLSVTSYS SFAFHKFSVAVYNISNLKTVD AKFPTTRYCYCLNNTDLSDF ALLVDIGNSTSYLTFKSTSL SVNQSNESDCIFCVMTGKSGR NLSDFWEIEEKYPINIYFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIGGPPPLGNQSPSSCSL LHEKDPPTTSGPQTDPKKHLT NFKSAARPTFLGQGQVPLNPF FTLS/EQVLLS*AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPLLCVSSLFSLASFTM GAFTHGTQTPTSPTKATAPRYPQ TGDLSAEWFTTAGEEPVLVPRP
15056	45424	B	15143	1	930	
15057	45425	B	15144	401	1093	
15058	45426	C	15145	1	843	
15059	45427	A	15146	1	498	
15060	45428	A	15147	112	669	SLQGRSLSDYTPTFQGCQTQGC LPWSFTLCSKSRFSGEGTRFKR IKACYHSPATAWPFKAYKLSLQ FPHFTRCKTRQALQVSSSEAPY QPNCFAYPFRGAEPHISPLNTS LHNPLFCSGSQTCFLY/SLCTL HPSLSLSLGLTLPIRLSKPLPGL YCLKSSQTAITSVKPKFLPHLL PISA
15061	45429	A	15148	957	1100	

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15062	45430	A	15149	303	2028	LGSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKHELTNFKSD KGD MFYPWTQN/YQCRSRTGK AAFPWCLITAGTPL*LYTHVSR VSDHAGMPALVLHP*RQVPLF WGRGKLLLRPS*VPILPQPPLL HPIIFLSPPLTPGPAYSFVL*LA LPHLPSNLLKRWLEPKA*SSM/ TLKGLKPVITRLQHGLLKPTN SPYNSPILPVLPDKPYKL VQD LRLINQIVLPHPVLGIHGLTSSV RRDAGQDLKRDRAEFLGDEV HHPHRRRIAEARRLLQGHEFDP LHRLIGQVLEGEARYAPPVEQ HHRLAPARRTGQRLHPLEQFG QAGRAQRNRNLGIEHRDLDRP DDGAGNALAGDGDFFRGCLFA GIGIRPRYCRYRQSQDDRRPSH AAPRPRALPIHPRPATPIADV VMFSVAIMSQRLRLVLRHIDGIS RWPPAVVFITDVKIWLVPYSD CRIRSNDRDDMQGEAPAMSMN AAARVGDPIGHISFSQGLFGEAL DGLFFARRSEVDMRAGNLGRLI ARGLSGGRWTPADGQLTLGSR DVFIGPPATMTIRSTGQCROH
15063	45431	A	15150	653	1076	RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCTPTPYFHDPTFPPLFW KELATSARNLATRPNACSPGF LLSCVPSVRDPTGNRTVQLTW QPLPEPLELWPKA/HLTDSFPDL LGAAED*CCPIASESP*TSDIIG RDTLLALKVQTVVLQTACGE GHVAGNCGRPLETEGSLQLTAT KKLRDSVLQPKSPEFCQQFTRA WNRITQVPDETEAPAGTYAAQS GDLPWEINPLSSCSLLHEKDPP ASGPQTDQPKHELTNFKSGFRG VRPRRDACLGPSPLAASPAFLG KGQVPQPLLSVSLPLLRLSGGQ ETPNPFSFTLSGKSAFLEEQVPQ PRISVPQSLISTRPLISVAQSLIS APQPLISLCPNPLFPCPDLLSLHP NPLFPRPNPFAFLEGACYKCQ KSGHQAKECLQGIIPKLRPICA GPHWKSDCPTHLAATPRAPGT LAQGSLLTDSFPDILGLAAED
15064	45432	C	15151	234	449	

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15065	45433	A	15152	2095	2663	LGLGDLPWEINPPSSCLLREKD PPTTSGPQTYQPKKHLTNFKSA CFERIKACYHSPAKAWPFKAYK LSLQFPHTCLKTRHAI/PS*FSD LCLINQIVLPIHPMVNPNPYTLIC SIPPYTMHYSVLQIRAFFTIPLH P*PSLY*VSLGLTLTPIRLSKLP GLHCRKASQTPITSVKPKFHP HLLPIST
15066	45434	A	15153	678	1189	LGSGLPWEINPLSSCLLCEKH PPTTSGPQTDQPKKHLTNFKSE TKETCFIHEPKTLAPVTD*GRQP SLGV*SLQGRPL*SFHSIRVSD HAGMPALVLHP*RQVPLFWGR GKYPNPFSPCLLPLLCFSGDRG KYPNPFSPCLYSFAFLGTGQVP QPLLSLSLPLLCF
15067	45435	A	15154	649	1428	QCISELQFLLASTVRQTPATSPA HKNFQTPELQRPGVPPEPPTG ACYTCRKS GHWAKECPQGIIP KA/HLTDSFPDLLSLAA/ED*HC PIASEAPETITDAELPVTLTVEA HLHPGEINSHVAHTKPVWWSL HRDAHEIWCCDSRGTSLRRPI PCPPALCSVTKIHLRPQVLRPTS PRNISPINPAAPHQAE LGPNPS/ SSLCSSLT*SFYHLPSSHLVWLT VSFRD
15068	45436	A	15155	240	1208	LRSGDLPWEINPLSSCLLREKD PPTTSGPQTHQPKHLTNFKSC KQ/DLFLSSPSTLTIPQLSPFN LGATLQSLPSLNFNSFHLVETK ETRFIRGPKTPAPVT/VLGRQPS LGV*SLQRCLSDYTPTFQGCQT TQGRPLPWSFTLSGK/CPLFWGR GNTL*KD*SLLSLACYSMGLLN PINSPPFSSHFTCPKTRQAVTS* VQDLRLINHIVLPIHPGGAQPH TLFCPQYRPVVLPIILFVYVKHA FFTIPLQPLIPSLSLPSRLTLTPI RLNKLPLGCCCKAFRDSPHYLN QAQISSSVTYLGIILIKAHVLSL PIVSDW
15069	45437	A	15156	1174	1623	KFGLVQLTLGKPLPELELWPK A/HLTDSFPDLLGLAAED*HCPI ASEAPYTTTDAELRVTLTVEGK SVPFLNTEATHSTLPSFQGPLSL ASITVVIGIDGQASKPLKTPQLW CQLRQYSFKHSFLVIPTCPVPLL G*DTLTKLASLTIP

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15070	45438	A	15157	1	1610	MGLGKSLCILKDAVLALREIKG ISFYQYAPNTNRLWGYRQAKQT QHLSGISTLDCPQRYNGDDTGS VWALEPSCMLWACPLVFPSEIY YFISEDVWKHLDAQEKFAAVM GPSRRTSVRAVWKGNVGLEPP HRVPTGALPRVAVKRGLSSRP QNGRSTYGLHCLKDTPQEDW LVSVLPEGSRVGVDP LIPTALG HGRITFLKVLDFQGPAPCPAA MGVRLMAGPQCVSDDYWKKM AKVLRSAAGHLIPVKENLVDKI WTRDRPERPCKPLLTGLDYG SWKDKVADRLRLKMAERNVM WAFVVTALDEIAWLFNLRGSD VEHNPFVFSYA IIRD*ETFMLFI DGDVRIDAPSVKEHLLDLGLE AEYRIQVHPYKSILSELKALCA DLSPREKVWVSDKASYA/V*SE TIPKDHRCMPYTPICIAKA/VK NSA/ESGMRISDEKSAGNLTED PFYVIDRTLITGVVCNSTEKSS LMSVASADTAENLWHLFFHILP SERALTRKLRVLKLGPNVYSVQ NPTAQLHQQGGPHLGVA
15071	45439	A	15158	1	756	
15072	45440	A	15159	1	1677	
15073	45441	A	15160	1220	2620	GPTEPHTGELWLESGGCPSGK LPEEGTGSNLCCSTASAGDTQA NRVCSGPPTNHSRPAADRVPVR KINKQKTATSTSTKRTSTORPH PKVTNDHSSSPAREQNWMEIE FDELTEVGFRRWVITNSSELKK HVLTCCKEAKNLEKRHSLGK EPAALKGRQYVQDSSPADLR PWLCA TLKQYKPTVFSHSTVA VHPRAGFLNLSTVDQHPVLDEP IAEAVCIADTNKWSVQVATSQ RKVPHNLKLGQDVLVSSQVSSL LQSILQLYKLHLPA DFGVDILLD NNLKCVFQLGSILPVTFRSHDP YDGEPTDELRTAACSPDTEQLA RQSGTYPVSLGQATVLEDSKA ALPGLGPTLMAVTVTTEAAV DMVVGDRGEERGGLVAPGTR GLTEEIFWPVPSRWRSSHPV VAFITLAKYGPTSSPPVFHHGPN IIRHGAQGAASAGDSGSSSRCD RLPCRQNA

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15074	45442	A	15161	666	1536	FSSAGDTQANRVCSVPPTNHSR PAADRPVRRKVNKQKTATSTS TKRSTQRPHPKVNDHSSSPA REQNWMEFEDELTEVGFRR WVITNSSELKKHVLTCQKEAK NLEKRVVNCLTRIT*P*RRTI KTLMEKNTARE/LHEAYTSINS WINQAEERLSEIEDQLNFIKRED KITEKMKNSTTVRVAASMQSK LLQGVAAEEGPLRLTRSAFSAEI SMCHQWLFSTFGNGKSRNRYH CEKAHIEGNQLVEETGRAFKSR HRYGTGPLHKFEIHEYTELHHV LMLQGGK
15075	45443	C	15162	104	364	
15076	45444	A	15163	162	467	
15077	45445	B	15164	1	1122	
15078	45446	A	15165	188	456	
15079	45447	A	15166	485	1580	GEGYKADLAAATVECPICQQQ RLTSPQYSHIPQGDQFITW*Q VDCIGPLLKGQRFVLTGIDTYS GYVFAYPVCNASAKTIISGLTE CLIHCHGIPHSIASDQGHFMA KEVWQWAHVHGIH*SYHVAD YPEAAGLIEGWNGLLKSQQLQC QLGDNTLQGWGKVLQKPMYA LNQHLYGTVSPATIHGSRNQD WNGSSRLGWFTILFTAPRREP GTYIASDQRTHFMAKEVWQW AHAHGIHWSYHVADYPEAAGL IEGWNGLLKSQQLCQLGDNTL QGWGKVLQKPMYALNQHLY GTVSPATIHGSRNQGMVEVA PLTITPGDPQAKFLLPVPMTLCS AGLEVLVPEGGTLPPGHITPLN
15080	45448	B	15167	10	2352	
15081	45449	A	15168	2	497	WKPIAMRKSRRRQEKLLPVQK EGQPKEGEREEGGPVQAQKVP NRLHLHWT/HLPSPFQLPLLLD SLWRALKFVVLAEIVKMIRFNG VLGKCEAIRAQLHEGGPPLPL AVFHNRLQIVACRSISARLRGS PPPKSNNEQSSSLDRLTDSQRL PPLSRNAQQKG
15082	45450	B	15169	1	1911	

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15083	45451	A	15170	1	1569	MPIGKVGEYYIKGLTRATKESE QQSSALELSSDRVLYLNEKEPGD QPWNAAFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPS TLNPSNWSLTLIIQCKQEGFYS PSMRPRVVPKRGSA PKVRAEEN AALPSRCPPGPLPVAQPRGLLM GAHVSSAPAVGVGAASCHRLC PGFPDRPRPTLRSCIMNAVVG CDLRGQVYDPTGGWANEGTR DL SAVQGVPNHPGGRPCPTPOS SRQLPVVSRPPVVRPGGEAPPP LDILPAALALHQSLTTPQDPRE DRPSPADLWAQDSWVGQPQEL PVGSRVRTGTGEPDTHSGSVCTS RQKKGDSGPLARESSVRVILQG PSSAWMMFPEYTPGPRARAGT AVVGAMARQTVNVCLTKVRL QHPEGIPGGGRGPLVPKPVCTC/ IVDVKGSRVVWHVHICMSMGC RHVCLCGRSVGSRMCTAGQT PKLARQASIELPSMAASSTKSW WETGEVQAQSAKTTPSCKDIV AGDMSKKSLWEQKGSKTSST IKMDSVTT
15084	45452	A	15171	328	641	LLMRWSLPSAPRGFSCSCLQP QYPCRTESWPQTEPVSPVSHR LLVLATAMLGSSME/RLAG*LG GPASGLDGLGVLFQPLINLGDG QVWLGFLHTVTLLYGAV
15085	45453	B	15172	120	1458	
15086	45454	A	15173	1	440	IQQDSQAPLYSIKETQRANTYL VEWEPGAETAFKTLKQALVQA PALSLPTGQNFSLYITERAGIAF GVLTQTRGTTQPPVVYLKDGEP IEHDYQQIIAQTYATQDDLLE PLANPDNLNLYTDGSSFVVGIR RAGYAIVSNVTVLE
15087	45455	A	15174	288	376	NHWLLLTMDPRIQQDSQAPLY SUKETQRA

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15088	45456	A	15175	777	1548	SKIQRDSQAPLYSVEETQRANT HLVEGEPEAEIAFKTLKQALVQ APALSLPTGQNFFLYITERAGIA LGILTQTRRETPQPVAYLSKEV DVVAKVWLHCLRDGEPKHDHC QQHVIQYAADDDLEVLPLANP DLNLYIDGSSSFVENGIRRAGYAI VSDVTVLENSLAAVTLQNRQG LDLLTAEKGGICTFSGKECCFY TNQSGIISPLEDTTITAGPFLHPI QQEVARAIIGQFPTAFGVSCLE GRLRGEASWTSWVE
15089	45457	A	15176	1	1359	MGPEPKNTHPGSCTCLACSSS HKGFEC LAVEQGSYTPVASPIV GVKENQEILDLELKYNQTRSA VTRCVLGAASTARIKQAEEGGR SRLAESSGLRPFVLELPALEHQ TPSSSGFELDLHQRLATWSQA FNYRLKDTLLASLLRFWDSD WLPCCSSVCSWPVGLHLVIIERN YSYQQGTETVVSWSWATGVSAA ASVSATIPINRYQGHCGFLGKR CFYCCIGECNHSDHQGPQTVAG SWARGVSATASQIQVDLGKFS DDPDRYIDVHLHTWRDVMLLL DQTLAFNENNVAAAAQEFQD TWYHRPVNDRMTAEQRDKFPT DIKTAAGIPWNHWWLLTMDPQ TQRDSQAPLYS\I*ETQRANTYL VEWEPEAE/TSFKTLKQALVQA PALSILTGQNFSLYVTERARLAL GVLTQTCGTTPLYQDELRRKKT LRRHDSSEGSFGNLEASAD
15090	45458	A	15177	368	5192	AAPAPQLGLGPCKLASHLLSQS HLSQSVRSEAEQKAGASPASSI QREPLFKDQLKAPLEQKRRSL LTVPLLTFRQKCGPGSPVVAR GGATDSWLVSSEFRLSDSTAPP TELRGQEATGITKPPASLHPQPH AWDWARGRDPRRHLLGTPELQ EHSEKTTTETLPADMGLRTW ERKEATAGQAAEGAAGGIHFE ATSLLRPSYVPQTQGALSTTY KEAKMDRDLHLTPILAAQQRAR GPRIHSFSPDEMIEPS

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15091	45459	A	15178	76	969	KKSTALVIDNGSCMKAGFAG DDAPQAMFPSTVGFPGHQGV VDMGQKDSYVGNEAQSRSIL TLKYPIKHGIITNWDNMEKIWH HFYNELHGAPE*QPVLLEDPL NPKDNREKMTQIMFETNTPA MYVAIRDVLSLYAFGRTTGIVM DCGHRVTHTVPIYEGYSLPHAI LHLDLTGWDLTEYPCILFSEK SYELPDGQVITIGNEWFWCPEV LFQPSFPCMESCRHQTINSIKK CDVDIRKDNVTLSSGTTMYPG IADRMQKEITALAPSTMKIKIIA PPERKFSVWIGCS
15092	45460	A	15179	1	451	
15093	45461	A	15180	130	227	LMKMKKV*RA*KEEERTTP AEDDFEKDLEWLINENEKSDAS IIEVYIANSIHNNYITKCFAIL
15094	45462	A	15181	104	1715	KEEERTTPAIVIPAAAFYTAY FLHKQKMENKDTDSKKEEY EDDFEKDLEWLINENEKSDASII EMACEKEENINQDLKENETVM EHTKRHSDPDKSLQDEVSPRRN DIISVPGIQPLDPISDSSENSFQ ESKLESQKDLEEEDEEVRRYI MEKIVQANKLLQNQEPVNDKR ERLLKFKDQLVDLEVPLEDIT TSKNYFENERNMFGKLSQLCIS NDFGQEDVLLSLTNGSCEENKD RTILVERDGGFELLNLQDIASQ GFLPPINNANSTENDPQQLPRS SNSSVSGTKKEDSTAKIHAVTH SSTGEPLAYIAQPPLNRKTCPS AVNSDRSKGNGKSNHRTQSAH ISPVTSTYCLSPRQKELQKQLEE KREKLKREEERRKIEEEKEKKR ENDIVFKAWLQKKREQVLEMR RIQRAKEIEDMNSRENRPQQA FRLWLKKHHEEQMKERQTEEL RKQEECLFFLKGTEGRERAFKQ WLRKRMEKMAEQQAVRERT RQLRLAERKSQQLQHLYMSE AKPFRFTDHYN

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15095	45463	A	15182	881	2040	MKAGWRQTQHLHDAGQLLHLI LPGEQGVARVQLRRDAAQAPH VNGHVVGVAQDHFVGSVEPA LDVRVYCGGKTGGKQREEREG RCGVEILMVGERKMENKETD SKESEYKDESEKDLLEGLTNEN EKSDASIIEMACEKEENINQDLK ENETVIEHSKQLSDPKSLQDE VSPRRNDPISVPSIQPLDPISDS SENSFQESKLESQKDLSEEDDEE VLPSSNSCVSGIKKEDSAAKID VVTHSSTGEPLAYI/ASTYKLAY IPPLNRKTCFSSAAISDRSKNG KSN/HGQSAHISVTSTYCLSP* QKEL/QKREQKREKLKREEEQ KIEEEEEKKRENGIVFKAWLQK KREQVLEMRRIQRAKIEIDMNS RVSKTSLKNKFIQI
15096	45464	A	15183	873	4292	MVVS LGRVSSLSEDSPTGRVG R*VDCKVDRSIWAGVWISEDAP SEA*EIGGLGRK*MLSGGPQSPS KHVHIL*DQDSSSIPEPMGPPCP PHAPGKEPGTSCSIDTDGKLSG VSGDDS*T/GTDGGESEIILLPQ *QLPVTLPSP.LP.G*VRYTSR SRSRSTRDPGRKSRPISGLRGLC GDGATS/PLTPRHAPARDVQ/P VSMFAFGADR/GDGRRGGASQ/ PAPPGPAVPRPCAQYSARAMPA SGRRRES
15097	45465	B	15184	1	2214	
15098	45466	A	15185	3	361	
15099	45467	A	15186	1	1035	MKIHKSGGLKATPQLYASQFSG VAILATWGPHRPRNSSTSFSTQS KLRRPDESSVDFQKMLCKEAT KKSKKEKPGMAFPQGHILFSDV AIKFSVEEWKCLNPEQRALYRE MMLENYRNLES/VG*LFKIHHDG VLINRARQYRSVPHRDIGKT*FL LPRNQERYSL*VSVARN*KK WP*STHNRNQRVN*VHTGEKP QKCNCGKTFSSQSYLQCHHR LHTGQKPYK*E*CDKVYSCRSQ LKTHRIHTGEKAYCKVCEK AFWDNSCLSCQKRVHIGKPYT ALVMHKAHTEKPYTCNECG KAFSRKANLALYHRLHTGEKP YKCECDKVYSRRSHLERHK
15100	45468	B	15187	1	1347	

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15101	45469	A	15188	1	1446	MWRETKRYAAVLLI.TPHYSAS LLPDW/PNLYLHQSGHHVPGVY LKFGSSNPIYPCVDSAKTVFPN APLHDRVQSVRRMGPFKGVFR KVFSNLGFEYSLSTWATMGSPG SLGVSPFGKTLFVESASGSLDA LWPTVEKEISSHKNYQKHSEKQ IYDVRIELTGLNALPNISLNFYK NSVSKLLNRKKGLIHLQPFILR LCVSLHKNREENLGITIQDVAM RLSALPNIVCRLYKKTASEVLK EWSTRWDEYTHHKEVVSQKALP TL SVKIYKKNICQLLNQNNGNP SEMNALITKKS VKSASGYLESI AALVEKEISSYKNYTEAFYNLL CDVYSHVTEMKLSSEIQIGNTL FVESASGVWRALRPRGKEVNDI FIDQIANSVLVDSSKDICKRFEA CGAMVKKENLHIKTRQKISEKL HWPFGAPRLTSLTQPEKTGKGE HPGAKARGELSGAPPLJHTRKL SLMSNVETLLLEKLGQYTGAI
15102	45470	A	15189	1	966	
15103	45471	A	15190	157	531	GDHTTFLCLLMVNAEFKYNFK TIIS*DLLKKDGGQYGHFTIFFRS MSIGCFSIYLCIFNFFHQCFAYF LVEIFTFLVKCIPQVDSIEDTTFG HPEEATPHPFSFFMRLEQFSHIF SSWPVSFTAH
15104	45472	A	15191	9	494	PTDRPRPRALAGARGPPGRAPR VPPAGGPRPSQYGHGGRPNPR HGWHDAFCPNNTPYR/ERPLDS RYLTPGPLDMRGDSGFRTGRGS DVGSLKPTDTRRNGKIYLNGS/ NVFYYQRLHPVHRGDGARRG FSGRCTCLHRMVC*YEQTGHQS DQT*KARSAYG
15105	45473	A	15192	1361	2038	
15106	45474	A	15193	1376	1906	LAFPDGMASLIMMSLPAMRTL AWAMAVSGNCIPEGQFSALSC ADFGISPKLIL*SSSAPNLYLAMG ISCPRADDLPEAGTAETDRACR SIPQYGTDLGWYPATAAGPQSE SVQGAV*PHRYEAG*ST/VWKP LKKK*KPLPRR*LARWQMRFR KPSPLTTSCLKTCA WRFLDFRW LE

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15107	45475	A	15194	1	1388	MIEHPRRRDNYRQSGPPVADKP TTKGEPLISDIVSDAQANLLIP VDETPPVINDEQSTSTPLTTAQT MALAAVADKNTTKDEKADDL NEDVTASLSALFAMLPGFDNTP KVDTPSTVLPTTEKPTLFTKLTS EQLTTAQDDAPGTPAQPLTPL VAEAQSKAEVISTPSPSISGVT RSKMRQREWLVLPEDSLVIRR SNKTSQLPAFNVPLSAAKAAAS KPWRASNTACRNSRPSKVCSAE GEQWFSASGRGEIHSQSPARDM AQMCKLAAEGHFAEARVINQR LMPHLNKLFEVNPPIPVKWACK ELGLVATDTRLRLPMTPTDSGR ETVSGDETYLEAAPLAELHAPA GMILPVTSGDYAIPVTNGSGAV GSYSAITEPGAGSDVGSLKTTY TRRNGKIYLNIGS/NVFYQQRL HPVHRGDGARRGFSGQTCCLR MVC*YEQTGHQSDQT*KARSA YG
15108	45476	C	15195	1	1905	
15109	45477	A	15196	285	1706	YARVHSGRSSIRRSIPVSIIRSSI RGCVPVHHCIRSSIRRSIPVDHL YQIHTKKHTRCFVSDHPYEE APDYSASLLPDWLPVPSKVVVI TYPGFTSICGYTTSSKACFSVF AWCFTSDVPGRFSEDEDDSE MWSLTALMGVMGGWKTARS EVSILCTSSKVIHSSYPYADRA FQVWSLDARFAHINKPFGVDRF SGAEPSRAITMYGVKVLNRPA TGTARHLVPPDVPVHPHGGESN KPRVQTTVSSGISRLSIPISASAL QNVDPKTHDISNITDTVYHCPL SQSSRWYWRFPVPRSPLNNGQ TAVRPGGRAGAAGGPLSEYS GSGFGVMKWTKDQLTVTKV HHLPEVVEFLYYKQGGWLSVL FGNDERKLNHYAVVYVLSRE KGTKCWI/TDSMDYRQR/PAPT NDAETYEFINELGARKTTVPPI GPLHVT/DEPGHLRLFVDGENI IEEANNE*IHTQC
15110	45478	A	15197	3	1396	
15111	45479	B	15198	1	1399	

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15112	45480	A	15199	283	796	FVGVKSAGNRLKTI DELANESR SSVGLTQAALKTLESSGAIRIER RGRNGSYL VEMDNKALLTHVD INNVCAMPLPYTRL YEGLASG LKAQFDGIPFYAHMRGADIRV ECLNGVYDMAVVSRLAESY LPQKGLCLAL*LGPPPYVGE\YQ L*QVKAKSEYVKRVGHV
15113	45481	A	15200	48	3376	
15114	45482	A	15201	49	681	DPGADRRGSVWGLSDLRNTYN ALYLTHSGRLSECP TPANEEKE PTNHNRTLNTQTQKEKKKTRT KDCTTRNK NSTRPGSGIAGPSY YTVAGPPSAIDPRWLRPTPPAL DPQ*MPHTSKRGKRADQSQPN ANKPNTEREKKDKNEGLHHKE QEQQRP GSGIAGPSYYTVAGP PSAIDPRWLRPTPPALDPQTEPL IFQQL EIDHYVAGLTHEVMSLS HLTLVMRWGSVSAHLAHWA RCRWISTELTPNSITSTSSPLKD CSSSPAMEQSWLENDFDELTD KKTCLCDH
15115	45483	A	15202	3	587	
15116	45484	A	15203	3	774	MVLMAGFTAGNEKGELVVLG RNGSDYSAAVLAACL RADCC E WTDVDGVYTCDPRQVPDARLL KMSYSQAE MELS YFGAKVLHP RTITPIAQFQIPCLIKNTGNPQAP GTLIGASRDEDEL PVKGISNLN NMAMFSVSGPGMKGMVGMA ARVFAAMSRARISVVLITQSSSE YSISFCVPQSDCVRAERAMREE FYLELEESLLEPLAVTERLPIS VGSDGNPPPCGGISPKFFAALA PRPISKFVALCSGIPF

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15117	45485	A	15204	1474	1511	HS*VPANLYMELKACFTGA/NE KGELVVLGHNLA VSYFIALAAS LRADCCETWTDV DGVYTC DPR QVPDARLLKSM SYQEAMELSY FGAKVLHPR TITPIAQFQIPCLIK NTGNPQAPGT LIGASRDEDEL P VKGISNLNNMAMF SVSGPGMK GMVGM AARVFAAMS RARISV GLITQSSEYSISFCVPQSDCVR AERAMQEEFY LELKEGLLEPL AVTERLAHISVVG DGMRTL RGIS AKFFAALARANINIVAIAQGSSE RSISVVVNDDATTGVRVTHQ MLFNTDQVIEVFVIGVGGVGG ALLEQLKRQQSWLKNKHIDLR VCGVANSKALLTNVHGLNLEN WQEELAQAKEP FNLRGLRLVK EYHLLNPVIV DCTSSQAVADQY ADFLREGFHV VTPNKKANTSS MDYYHQLRYAAEKSRRKFLYE HNTFVSPHIRPLIERRGRSSTRD KWCARPSTERQQDNSAARILSC QQGNTSFEHTSSIRVGT TNSLN
15118	45486	A	15205	198	462	

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15119	45487	A	15206	31	1981	RWLMRGMGIALPAAMASTVSP STIAETPEPPPLSDW/LRASG/DV VVHLLGLDPHLSLLLSICLFSR SLIWIF*LQP*SV/ALAFQMGAS LFASNIGVIEGEGPQAKPL*CLT VSYFEMLNLLNAQGPCKGLSP CQCLSLQVMTMPEYLLKKRWTL GQRSQWPQMHSVFS*LFPE*A DIFAGAIKQPSGEGKYMRT G*NALVLFLLSGGLEVVHINIG CLRFQ*DISFYSDAFLAFNEVGG YESFTEKYVNATPSVVEGDNLT ISASCYTPRADSFHIFRDAVTGK GR*LPLKSSPGLFHIECVTFSRQV IVQRCL/CGKDMSHVKAACIMF LFV*WLLVLPWASLDSLLNSSP DMVACVVPSECVISTLSGLARQ CPATNQCLYPPAPGLRGLMLS VMLASLMSSLTSlFNSASTRTK AQWK*L*CFCLMFKLCCFLRLI FVLLLTVVSVVWVPLVQVSQNG QLIHYTEI***LT*ISFYFLNLI FFLLLLQGAFWGLMVGLAMGL IRMITEFAYGTGSC LAPSNCPKII CGVHYI.YFSIKVPFYITIANICL LLMHFCMVPVQLYRLCWVLR NTTLTRISSFVI*IFCNHLLIFVP DYPEKSRGCLCKAYDLFCGLQ KGPKLTKEEEEALSKKLTDTSE
15120	45488	B	15207	1	1392	
15121	45489	A	15208	57	1523	
15122	45490	A	15209	473	589	LPRQLALSCVVHCQTLVPAIRCI DWGWLF*W*SVTPVM

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15123	45491	A	15210	1	1297	MGKIMSSYQHVDLIVDCDFEA YHRQPSSGTSVVTGPSAQA TEKIVTYHWDQHVGDVVLNI YCVINVL DHTVKAVIDDRFMG GITTINLQLMAIIVRYFFASGSA YIVAMLPVFAMLANVSGAPLM LTALALLFSNSYGGMVTHYGG AAGPVIFGVGYNDIKSLCFDER TRIDVADTYASNWRSRCNQITF NGECPNTRQHIAAVRRGIDTLL MNDYLKQIIDI STRIAGTANN GDFGTGQWITAANTVNFQIVAGT HNCHQYFIALRLFILKYIQDR AREGLKQRDLAEALSTSPQTVN NWIKRDALSREAAQQISEKFGY SLDWLLNGEGSPKKDLESNIPP ESEWGTVDADWKNTPLPDDEV EVPFLKDIEFACGDRVHDEH NGFKLRFSKVVPQPRVGC*QG* G*LLYLDV**GDPLEST
15124	45492	A	15211	62	301	SWMSSPRAFFSSCTLETAAPTR MATALTSAACRLPPAAGSGSP WAPAPYRWRARRRTGPMSSDR Q*RTSQPCPEAAASR
15125	45493	A	15212	1	1665	MQD SAHLRRLLPPAASRRVWLA LGSCPLPLESSPAHRA YERPSVA HQPAVPGARRSLEVPSEVPLTV PALTPPRIPAMLTAVCGSLGSQ HTEAPHASPPRLDLQPLQTYQG HTSPEAGDYPSLPQGELQSLPL GPEVDFSQGYELPGASSRVTC DLES DSPLAGPFSKLLQPDMS HHYESWFRPTPGAEDGSWWDD LHPGTSWMDLPHQTGALTSFG HPGALQAGLGGYVGDHQLCAP PPHFAHLLPAAGGQHLLGPP DGAKALEVAAPESQGLDSSL GAARPKGSRSSVPRSSQTVCR CPNCLEAERLGA PCGPDGGKK KHLHNCHIPGCGKAYAKTSHL KAHLRWHSGDRPFVCNWLFCG KRFTSRDELQRHLQTHGTKKF PCAVCSRVMRSDHLAKHMK HEGAKEEAAGAASGEGKAGGA VEPPGGKGKREAE GSSMASSPD SPCSCDCFVSVPASAIPAVIFA HELGP TPRGAGGGVCPRRHS HSWEPAPGL*AVGGGGGASGQ AGDRGCHA*EAGRS/SCSRGS GL*RA GTS*ISASS

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15126	45494	A	15213	3	471	GRPSSPGVHGSSQTPTAHVGSF PGCGPIPPD/ACRRSKIRPGGW GGVGG/CRDGRNSR/DLRNLPC PFLFLPGP*AAAPSPWPAAAGA APCGQCLDGWPHSYSHGHSSA AGRGGICRSPLLAGELRPPGIQ YNGRTEVRGILSGSPCPPFSGAG
15127	45495	A	15214	3	449	PHQDLEEA MVLL*PPSP/PAWPT MRTRKRPSSKVSSTSRPLKXSIM TTYAVPSRAPTPA*PSASKPTNA FS/HMVGSEPRSHAHLDDGRHRD SR*RKPRPLSGPRTLGGKSLRGS AGAGRGGVPRPRPLPENLDAPL WNSPGNSAGAAVQLA
15128	45496	A	15215	26	1126	EGPSSEAAHPGGTPREQDGAM DPARKAGAQAAMIWTAGWLLL LLLRRGAQALECYSCVQKADD GCSPNMKMTVKCAPGV DVCT EAVVAVETIHGQFSLAVR/GCG SGLPGKNDRGLDLHGLLAFIQL QQCAQDRCAKLNLT SRALDP AGNESAYPPNGVECYSCVGLSR EACQGTSPPVVSCYNASDHVY KGCDFGNVTLTAANVTVSLPV RGCQVQDEFCTRDGVGTGPFTLS GSCCQGSRCNSDLRNKTYFSPR IPPLVRLPPPEPTTVASTTSVTTS TSAPVRPTSTTKPMPAPTSQTTPR QGVEHEASRDEEPRLTGGAAG HQDRSNSGQYPAKGGPQQPHN KGCVAPTAGLAALLLAVAAGV
15129	45497	A	15216	1401	1983	AQRAQALECYSCVQKAD/DGC SPNMKMTVKCAPG/VDVCTEA VGAVE/SHPFWIWPRPFNAAPP LSAWPGPYDTALQARPLY*QL QARGAES*ELVH/GQFSLAVRG CGSGLPGK/NDRGLDLHGLLAF IQLQ/QCAQDRCAKLNLT SRG LDPAGTSPPVVSCYNASDHVY/ KGCDFGNVTLTAEPPTVASTTS VTTTSPQ

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15130	45498	A	15217	1	964	MNVKGD TQGNTRVRVDNIGG VGAQTVNGIELIEVGGNSAGNF ALTTGTVEAGAYVYTLAKGKG NDEKNPSVYRPEAGSYISNIA AANSLFSHRLHDRHSLQPLKI LVTGGAGFIGSAVVRHIINTQ DSVVNVDKLTAGNRSLADV SDSERYVFEHADICDAPAMARI FAQHQPDVMMHLAAESHVDRS ITGPAAFIETNIVGTYYLLEAAR NYWSALDSDKKNFRHHISTD EVYGDLPHPDEVNTEELPLFT ETTAYAPSSPYASAKASSDHLV RAWKRTYGLPTIVTNCNNY PYHFEKLIPLVILNALE
15131	45499	B	15218	44	405	
15132	45500	A	15222	1	498	MTRSLLSVFEEADAGTLTDYTNQ LLQAMQVRVYGAQLNLLHTELA KQLAETQWFYLSYNSEKRISQTL SAMWRGRAAAQ/TQGHWWVG MVEAVCSKVSTLKDGLGLASN EHDLSMAKYSLPKKENEKL AAFGQPTWCDPAERYGVFLPV GPDPGAKSAPSPRDRASTL
15133	45501	A	15223	1	1224	
15134	45502	A	15224	1	1353	
15135	45503	A	15225	1	2580	
15136	45504	A	15226	1	3117	
15137	45505	A	15227	1	1260	
15138	45506	A	15228	1	2142	
15139	45507	A	15229	1	1413	
15140	45508	A	15230	1	4049	
15141	45509	A	15231	1	381	MLMLNIGFKNFQFEHLKCSHGS YSEDIGFPNAGALSGAMFLEE KHLLFGLKEERLRASIRRESQ QRRMRKQHQRLSASYWNLI DTMRRRKARSP/YSLAIAIKNRY KGGIRDQKPSYDSLNLCTMT
15142	45510	A	15232	1	467	DHSSSPAREQNWMEFDEL EVGFRRWVITNSSELKKHVL TQCKEAKNLEKRLGELLTRITSL EKNINDLMELKNTARELHEAYTS INSWINQAERLSEIEDQLNEIK REDKITEKMKNSTTVRVAASM QSKLLQGVAAEGPLRLTRSAF
15143	45511	A	15233	1	1140	
15144	45512	A	15234	1	2640	
15145	45513	A	15235	1	714	
15146	45514	B	15236	1	546	
15147	45515	B	15237	1	735	
15148	45516	B	15238	50	1603	

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15149	45517	A	15239	1374	2220	QAENSHININKKDVHSETPSEG HQRKRPKDHSSSPAREQNWME N\EFDELTEVGFRRWVITNSSEL KKHVL TQCKEAKNLEKRLGEL LTRITSLKNNINDLMELKNTAR ELHEAYTSINSWINQAEERLSEI EDQLNEIKREDKITEKMKNSTT VLVSTWGSQLEQNNLPHIISPLF HSTHDLNISFYGGCLLQACSSK LLQGLAEGGPLRLTRSAFFAA KLCLTKHFLPTMILIKSRKTTP DTQPRRLYLLQGVVDQTSRKG PTALNIRQKTFAAAPPHR
15150	45518	B	15240	1	1311	
15151	45519	B	15241	46	212	
15152	45520	A	15242	3	371	EPLPPEPPAVPSEVELQHLRKEL ERVAGELQSQVKNNQHISLLNR RQEERIREQEERLRKQEERLQE QHEKLRQLAKPQSVELKISQEV QSLQQQPDHFLGHLQQYVIAT LSAARWAAQQLD
15153	45521	A	15243	392	558	
15154	45522	B	15244	52	689	
15155	45523	B	15245	400	603	
15156	45524	A	15246	5	1158	RKFWRWMVVMMAAQHSQAAQ GQRR**VSKGP**PGPMGGPVL GHWWHSGGISLAVPSLPPGKS SVFLFLFSASFMDKMLNPGTVSP RLIFGSYDDGFLVETVVKFDFQ LWQKTPLHRAAGERRRAEQRG KLSFVMP

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15157	45525	A	15247	1	1808	MAEETQHNLAAAKKKSATGF HREGPTSSATLKDLESPCQERA VVLDSSTVKISRLKNTIKSLKQQ KKQVEHQLEEVTPDNLPVWV GLSWGIGGILGACLLCHLCLP LEKKANNERQKAERELEVQIQT LIHQKEELNTDLYHMERSLRYFE EESKDLAVRLQHSIQCKGEI.FS ALSAVIATEKKKANQLSSRSKA RTEWKLEQSMREEALLKQVLT QLKESFQQVQLERDEYSEHLKG ERARWQQMRKMSQEICTLKK EKQQDMRRVEELERSLSKLN QMAEPLPEPPAVPSEVELQHL RKELERVAGELQSQVKNNQHIS LLNRRQEERIREERLRKQEE RLQEQHEKLRQLAKPHCAFSSRS *TMRTRAHLQLEQQVKELQE/Q ALARVFLQVELKSQEAQSLQQ QPDHYLGHPAAEHLEAASQQN QQLTAQLSLMALPGEGHGEH LDSEGEAPRPMPSPVEDLES EAMVAFKKSAGASAQEKQAL QEQVKEQRVCCQRLAHPVASA QKFEPAARPGAPGPGGESSF MDHLKEKADLSE/PGEKRTLH P/PTG/GDRRHQKTHHLLSEPGG CAK/DAALGPQHQAQAGGDD
15158	45526	A	15248	2085	2700	YPGKRGLEWT*ANSNRPAAG PDE/SSSLPATEQSWMENDFDE LRKEGFRRSVITNFSKLEEDVQ THRKEAKNLEKGLDEWLTRINS IEKTLNDLMMEMKTMA*ELHDT CTSFSSRVQVEERLSVI*QDM NEMK*EEKFREKRVKRNEQSL QEIWNYVKRPNLHIGVSEIDR ENGTKLENTLQDIFQENFTYLA RQANIQIQEI

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15159	45527	A	15249	378	1744	QTERNSININKKDIHTKTPSVRH HHQRPKLHKTTKMGKKHSRKA ENSKNQSGLPPKECSSSPAVE QSWTENEFDEFT EEFGRRIESQ MNEIKGEEKFREKRVKRNEQSL QEIWDYVVKRPDLRLIGVPDSDG ENGTRLENTLQDIIRENFPNLAR QASIQEIQRTPQRYSSRRATP RHIIVRFTKVEMKEKMLRAARE KELKIKKLTQNCLETTWKLNNLL LNDYVWHNEMKGEIKMFFETN ENIDTTYQNLWHTFKAVCRGK FIALNAHKRQERSKIDTLASQ LKEIEKQEQTSHKASRRQEITKI RVELKEIETQKSLQKINESRSWF FEKINKIDRPLRLIKKKREKNQ IDTIKNDKGDITTNPTIEQTSRE YYKHL YANKLENLEEMDKFLD TYTL SGLNKEEVESLNTSITGSE VEAIINSIPTKKKSRTRWIHSRIL PEVQGGAA
15160	45528	A	15250	935	1269	LIEGKLTERN SININKKDIHTKT PSVG/PPSSKTKDRSSLPAIEQS WMENDFDELTEVGFRRSVITNL SKLKEDVRIPHKEATNLEKRLD EWLTRINSIEKTLDDLMEKTM
15161	45529	A	15251	401	497	KTFSPFYFS*RRRTVRDINGFTE Y*EPEKLLG
15162	45530	B	15252	220	940	
15163	45531	A	15253	1	1476	

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15164	45532	A	15254	1	2423	MNGKNKNTIYQEPTVCQALHW TLARIGKEEPRRGQRGEGLLCS RERQPRGLSSPGTAAPAAPAP TPPALPGHRTSRGSPGEPILR RGGSADAPGRVKTWVNRPAF VGKCLGDGSDTACDQAMKG QRGSNRKRKTSLSLTFPTSSDM HAGGLSAAHPCAHSRAPPPASP SPYKGLGTRTDGLTDSRADSA ASGARALGVGGPQPSPRRAP PRPVGADGSSRGPPGRRRVER RGPATQPGDSRALPEPRGVPAV HPAGSGSEWERPPAAPSPPEHR DKMLPGLRRLQLQASARRPQFPF EAAARWVWSPCFSSGTLCPSPFQS ERPLLPFGGASFPQTTLHQRCLCP VAALHSGSGKGQKWQQSHCYA AAVMEPPAPGRSSSLQGPLS WAGGAPASACLLMLLALPLA APSCPMLCTCYSSPPTVSCQAN NFSSVPLSLPPSTQRLFLQNNLI RTLGARHLWVQPAHPVALLQQ PLHHLPGHFPP/LQALEELDGLD NRHLRSLEPDTFQGLERLQSLH LYRCQLSSLPGNIFRGLVSLQYL YLQENSLHLQDDLFADLANLE PTSLHGNRLRLTEHVFRGLG SLDRLLHGNRLQGVHRAAFR GLSRLTILYLFNNSLASLPGEAL ADLPSLEFLRLNANPWACDCR ARPLWAWFQARVSSSDVTCA TPPERQGRDLRALREADFQACP
15165	45533	B	15255	47	482	
15166	45534	A	15256	1	636	MRDPNTKRSRGFGVTCATVE EVDAAAMNARPCVVGRTVEPK RAVSRSDSQRPEDTEELHLRDY FEQYQKIEVIEIMTDQSGKKR GFAVTFDNDHSDMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQGRSGSGNFGGGRGGGF GGNDNFGRGGNFGHGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVYNNQSSHFPGM

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15167	45535	A	15257	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDLSLRSHFEQWGLTDCVV MRDPNTKRSRGFGVYATVE EVDAAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQGRS GSGNFGGGRGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSYGSGRRF
15168	45536	A	15258	1	286	
15169	45537	A	15259	1	1674	
15170	45538	A	15260	235	1370	KREGEGRLADTFVSLLSARGR RRRSIVKVSHPAVMSKSESPK EPEQLRKLFIGGLSFEITDES LSRSHFEQWGLTLDICVVMRDPNT KRSRGFGFVYATVEEVDAAAM NARPHKVDGRVVEPKRAVSR EDSQRPGAHLTVKKIFVGWH* RKTTFWGGKKRAKHHHLRD YFEQYGKIEVIEIH*LDR/GQWP RKRGFVFTDDPDSVDKIV/ QKYHTVNGHNCEVRKALSKQ EMASASSSQGRSGSGNFGG GRGGFGGNDNFGRGGNFS/ GRGGFGGTGGGGYGG/SVG DGYNGFGNDGSNFGGGGSYN DFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRN/ QGGYGGSSSSSYGSGRRF
15171	45539	B	15261	1	660	
15172	45540	A	15262	2	486	KMRQREARQGGK/VAPAPAVV K/KQEAKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVKWPRYIR LQRQRAILYKRLKVPAINQFT QALDRQTATQLLKLAKYRP/G DKGALAKLVEAIRTNYNDRYD EIRRHWWGNNVLGPKSVARIAKL EKAKAKELATKLG

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15173	45541	A	15263	3	845	PPKMPKGGKKAKGKKVAPAPAV VKKQEAKKVVNPLFEKRPKNF GIGQDIQPKRDLTRFVKWPRYI RLQRQRAILYKRLKVPPAINQF TQALDRQTATQLLK/LVAHKYR PTEKQEKQRLALARA/EKKAA WQKGTSPTKRPPVLR/AGS*HP VTTLVENKKASAGW/WIAHRR GFPSSLVVFLPALCREKWGSPY ICIIKGKARLGRLVTRKCTTV AFITQVNLGRQALLKLVEAI RTNYNDRYDEIRRHGGNVLG PKSVARIAKLEKAKAK/ELATK
15174	45542	A	15264	1	5796	MPRVEKNIPGRNRNSKGFEDPLE VTQDVTREWAKKVVWVWREKA SKINGAYFCEGRVGEAIRIRT MKMRQQATLTMTVDKGDNVN ISFKKVLKEEDAVIYKNGSFIH SVPRHEVPDILEVHLPHAQPD AGVYSARYIGGNLFTSAFTRLI VRILPPQENIKISNITHSSAVIS WTILDGYSISSITIRYKVQKGNE DQHV DVKIKNATITQYQLKGLE PETAYQV DIFAENNIGSSNPAFS HELVTLPESQAPADLGGGKML LIAILGSAGMTCLTVLLAFLIILQ LKRRANVQRRMAQAFQNVREEP AVQFNSGTLALNRKVKNPDP TIYPVLDWNDIKFQDVIGEGNF GQVLKARJJKDGLRMDAAIKR MKEYASKDDHDFAGELEVLC KLGHHPNIINLLGACEHRERGD RRHLENQVPTLILRFSNLSKR HTRRLYPEPGSEGPTPTPEPSLL AQQSEIKLHGGSEPLLIFRQTG SGVDLQQTPTNLQLRVLTVRR KTDKRKGHPHQKPCSSPSSKT KEGFRRSNYSKLEEVQTHGK EVKNLEKKLDKWLTRITNAEK SLKDLMEKTKARELCDECASL TSQFDQLDKRVSVMEDQMNE MKQEEKFREKRIKNEQSLQEI WDYVKRPNCLIGAPESDGEN GTKLENTLQDIQENFPNITRQA NIQIQEIQRTPQRYSSRRATPRHI
15175	45543	A	15265	1	2212	

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15176	45544	A	15266	1	743	PPLLIFRQTGSGVDLQQTPTNLQ LRVLTVRRKTDKRGHPHQKPI CSSPSSKTKEGFRSSNYSKLKEE VQTHGKEVKNLEKKLDKWLTR ITNAEKSLKDLMEKLTARELC DECASTLSQFDQDKRVSVME DQMNEMKQEEKFREKRIKRN QSLQEIWDYVVRPNLCLIGAPE SDGENGTKLENTLQDIQENFPN ITRQANIQIEIQRTPQRYSSRR ATPRHIIVRFTKVEMKEK/MLR AAREK
15177	45545	A	15267	1	618	EVSRRNTRTKTSYKQDMNTSK GF*KDTST*PVT/KERSSSPATEQ CWTENDFDELREEGFRSSNYSE LKEEVRTNGKEVKNLEKKLDE WLTRITNAEKSLKDLMEKTM ARELCDETSLSRRCDQLEERV SVMEDEMNM
15178	45546	A	15268	200	618	
15179	45547	A	15269	158	594	SGSSICCSPISTVLQPPLLTQRQT GSGATSSK/SPTDLQLRECS SSP AKEQSWMENDFDELREGFRSS NYSLEKEEVQTHGKEVENLEK KIDEWLTRITNAEKSLKDLME KTMAREQCDECTSLSSRRDQLE ERSVSDQINEMK
15180	45548	A	15270	3	1453	LSDELEAAQSIIIFAGYETTSSV LSFTLYELATHPDVQQKLQKEI DAVLPNKERSSSPATEQSWTEN DFDELREEGFRSSNYPKLEEV RTHGKEVRNLEKKIRQM/VTRI NAEKSLKDLMEKLTARELRD ECTSLSSQFNQLEERVSVMEQ MNMKKEEKFRKRIRKKEQS LQEIWDYVVRPNLRLIGVPESD GENRTKLENTLQDIQENFPNLA RQANIQIEIQRTPQRYSSRRAT PRHIIVRFTKVEMKEKMLRAAR EKEIQTIREYYKHYANKLEN LEEMDKFLDTYTLRLNQEEVE TLNRPITGSEIAIINSLPTKKSP GPDGFTAIFYQRYKEDLVVPFL KLFQSIKEGILPNSFYEASIIIP KPGRDTTKENFRPISLMNSDT KILNKILANRIQHIKKLIHHDQ VGFIPGMQGWFNIRKSINIQH NRTNDKTHMISIDAFAFNKIQ QPFMLKTLNKL
15181	45549	C	15271	111	269	

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15182	45550	A	15272	94	4505	YLDMMSFVQKGSWLLALLHP THLAQQEA VEGGCSHLGQSYA DRDVWKPEPCQICVCDGSGVLC DDIICDDQELDCPNPEIPFGECC AVCPQPTATPRPPNGQGQGP KGDPPGPIGRNGDPGIPGQP GSPGSPGPGICESCTGPGQNY PQYDSYDVKSGVA VGGLAGYP GPAGPPGPPGPGTSGHPGSPGS PGYQGPPEPGQA GPPGPPGPP GAIGPSGPA GKGDESGRPRGP ERLGPPIKIG
15183	45551	A	15273	1628	1832	RRRRKARERRRLAAEQGRMK EQCKDGFSE/QASGALKLMGSN EGEFKAEGNSKFTYTVLEDGCT KHTG
15184	45552	A	15274	1	362	
15185	45553	A	15275	1076	1240	LRQLL*LCPSWRLCLLGGWQL HLFF*RHFFVHLVSQRCSIAM SPSRRCFSLHL
15186	45554	B	15276	480	1167	
15187	45555	A	15277	3	379	
15188	45556	B	15278	13	369	
15189	45557	A	15279	112	1112	WPPASPSASVIRTVKEFALTNP KSSTKETERKETKAEELDAEV LEVFFHPTHEWQALQPGQACPC RNPTYGLNLQTGEREAKLQYE DKFRNNLKGRLDINTNTYTSQ DLKSALAKFKEGAEMESSKED KARQAEVKRLFRPIELKKDFD ELNVVIETDMQIMVRLINKFNS SSSLEEKIAALFDLEYVHQ DNAQDLLSFGGLQVVINGLNT EPLVKEYAAFLGAFFSNPKV Q/EWEAIEGGALQKLLVILATE QPLTAKKKVFLALCSLLRHFPY AQRQFLKLGGLQVLRITLAGE GHGGARRARGHTALRCPCHREK CSPRRRLS
15190	45558	B	15280	54	385	
15191	45559	B	15281	274	776	

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15192	45560	A	15282	362	1323	HQLGRSALLDTRTVSMQKAKN GDAVTEPQVA/ENEANGKDTA EVDLLTKELEDFEMKKATARA VTGILASHPCSTDVHIINLSLTF HGQELPSDTKLELSVVRHYGLI GLNGTENSMLLSAVGKHGVP EHIDIYHLTREMPSPDKTPLHSL VTVSSPRQRDDMSDGHLCAR RHTDIRDDSPDAPDTARSLAR STITTRRIFALATPSRTLQVCS ALAYTSHPAARTQLASTALTR RYMLPSPQLPSLRDHRRTNPLH SAVATIPHTTTGEADVSLLCIGL STLHYALVYHVSVLTA MSATDASIIFFPKR
15193	45561	A	15283	3	537	
15194	45562	A	15284	1	455	MPRPEKLGKTQVPLAECLTKD SFLGQKQASLGLPTFRDVTIEFS LEEWCQLDVTQQNLYRDVMLE NYRNLVFLVISS/HFTQDFWPD QSIKDSF/QRIILRTYARCGHKN LRLEKIVKVS MRKHQIIHTGKK PYKCECAKLLSPQLENMR
15195	45563	A	15285	1	397	FAVLMAHYDVQEEDPVLTVIT YMGLSVSLLCLLAALTFLLC KAIQNTSTSLHLQLSLCLFLAHL LFLVAIDQTGHKVLCSIIAGTLH YLYLATLTWMLLEALYLFLLTA RNLTVVNYSSINRFMKLMFPV
15196	45564	A	15286	191	1332	AJETQAITDNCSEERKTFNLVN QMNSMDIRCSDIQGDTCQPSVI AFISYSSLGNIINATFFEEMDKK DQVYVLSQVVSAAIGPKRNVSL SKSVTLTFQHVKMTPTKKVFC VYWKSTGAG/CSQWSRDGCFLL HVNKSHMTMCNCSHLSFVAVLM ALTSQEEDPVLTVITYVGLSVSL LCLLLAALTFLLCCKAIRNTSTSL HLQLSLCLFLAHLFLVIGDRTE PKVLCSSIIAGALHYLYLAFTW MLLEGVHLFLTARNLTVVNYS SINRLMKWIMFPVGYGVPVAVT VAISAASWPHLYGTADRLAF KATAQLFILGCTWCLGLLQVGP AAQVMAYLFTIINSLGFFIFLV YCLLSQQAHHKFTPEVPRQN HRLCQON
15197	45565	A	15287	263	397	GRPPAPAARVSGPASVSAG*KR VSAGSVGVRSMRRGSALLPPN F

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15198	45566	A	15288	1	278	MKFDHGRGQMOPKPSAEAVNS APQREPEGSILRAADPLVWAAK AMSASR/RGS/CGGSSADPRHTE RTPTPEPDADTRFQPAETLAGPK TRAAGAG
15199	45567	A	15289	5	545	SFMTEAKSSPNPAQQLSTQRP SESRRKVPSSSELQTLSCGLQRPC HPGRPGDPYYASASTRTRSPS ARHAVWGRRGCYPEA/AVRAR EGPHPTLAPASTYGLASPPRAD SAHRPRHRSLSRLLPNRKLGGG SADPRHTERTPTPEPDADTRFQ PAETLAGPKTRAAGAGGQPWD S ANASPP
15200	45568	B	15290	121	822	
15201	45569	A	15291	1	1308	MLRMVIGIEISNGQWSTPPCQVL HLEGNDIYNPKEQGLGNTCRW GWMAAGTRRNLCWAPFPFLNP VASLVLHSTIQIALQESKDRVL GTLINSLPVTSTDKANWSRLRA LEVGDGGGLVGLSPQVPGSGA MSRCPNCTRKLGSGISPTSSL AEEQGSVVKTHSHQGGARCSK EKGWQIL.LILVAGLCQLVVVV QNVGVRKIPRKYLAALRVAIGH ALAIERRRIRVDVADQAQDTDR DDRSFGRDRNRDSDKTDTDWR ARSATSDSDDDYPPRRGDDRF GDKYRDYDSQYGRGYWYER DGPCTDMDRYGGSGRRAFG SGY/RRDNDYRGGRDRYEDRY NRWDDGSSSRDDFSRDDCRY NDRRPPQRPKLNLPKHPNTPKGD DSSASTSQSSRASVFVGGAKPV DRAARETKVEEVLQEQDKLQ HQLDEAKLE
15202	45570	A	15292	2	293	
15203	45571	C	15293	56	298	
15204	45572	A	15294	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYL.SACRHPMEDSMDMD MSPLRPQNYLFGSLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS

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15205	45573	A	15295	3	1024	CGGIHSVLRGCSLEPAFFYLRSASFPTISACRHPMEDSMDMDMSPLRPQNYLFGCELKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIKVTLVATLKMSVQPTVFPWGAFEITPTQWSRLRLKCGSGPVHISGQHSFKLLEEDA\SEDEEEEDVKLALSISGKRSAPGGGSKVPQKSKTLLLMKDDDDDEED\DEDDG*WMDFGWMEEAEEKAPSERNPIRDTPAKNAQKSNQNGKDSKPSSTPRASKQGESFKKQEKTPKTPKGPSSEVDIAKMQASIEKGGSLLPKVEAKFINYVKNCFRMTDQEAIQDLWQWRKSL
15206	45574	B	15296	1	1107	MLASMGVVAEKMKYLSSPYQGHAFHTRJLSMTVNFQAQLWLPNEAGPTGDDWGGDTHGCPSFSPHLPRFIQKQPVWGTGRLLQEHFSCSKSLVPVPSRDIEAFHLHADLILNTLPSLVIIQIESHSEELRARVSTYESGEDTIQCITVTWKPKYGATRWKDPGSPDGPLEERLEDLSTRNNSIRLFRGCGYRVKQNSSQRPNKVCGLPDTGVLLQTKCGLVRNSQRSAPNTNKQH EELFSTAGIPENLSRRQEVLPGHGFTGWVGWTWKLTSSEGVTFHHLSATHKLSHASCRQGNFKPKGAMSVTRSTVHPHLAFLSAEINGKCGRPCVFLGIWAINCGMAILYERLSALVCVSVSERHLDYTMRFDFDIPSTLEARIGSPLWALSLHPLRSSTVTSSVELILPECTVAVLEIQYVFLGDTILFTTVGKARSCTRDRDGGRAQIMQVLQGGKGRELDAAPQEPGQLLREVRVVGVPFIPRARVDAWLVTVAVGSADEAHGLLGAAASSTGGAGASVDGGSQAVQGGGGDPRAARSGPLDAGEEEKAPAEPTAQVADAGGCASEENEVLREKHEAVDHSOREENEERVSALKENSLQQNNDDENKIAEKPDWEAEKTSERNERHLNGADTSFVSEDLFQLL
15207	45575	A	15297	1	1968	

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15208	45576	A	15298	1	2104	MKHLKR VWSAGGGLLHLTL LSLAGLRVDLDLYLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRLGVFPVPTSV DAWLVSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGG/CASEE NGVLREKHEA\VDHSSQHEENE ERVSAQKENSLLQNNDDENKI AEKPDWEAEKTTESGNE\RLH NGTDTSFSLAEDLFQLLSSQPAEN SL\EGISIWGD\PLPGISIDGHEF FKHIYHVNFQPRLS\QD\VNHL EAILLCPNNTFRDPTARTSQSQ EPFLQLNSHTTNPEQTLPGTNLT GFLSPVDNHRNLTSQLLYD LDINIFDEINMLSLATEDNFDP DVSQLFDEPDSDSGLSLDSSH NTSVIKSNSSHSVCDGAGYCT DHESSSHHDLLEGAVGGYYPEPS KLCHLDQSDSDFHGDLTQHV HNHTYHLQPTAPESTSEPPWP GKSQKIRSRYLETDRNLSRDE QRAKALHIPFSVDEIVGMPVDS FNSMLSRYYLTDLQVSLRIDIR RGKNKVAQAQNCRRKLDIILNL EDDVCLNLAQKKTREQAQC NKAINIMKQKLHDLYHDFSR RDDQGRPVNPNHYALQCTHDG SILIVPKELVASGHKKETQKGK
15209	45577	A	15299	2	342	RRFRVAAAAGVTA*AVVLSA RPSETWETRGR*RICPSSWP* GI*VNNG*K*RRHSVCQCSLWF PARCIKPYHSMARITQPGTRNKE NGPAGPTALDNVASSDDTGRH RPQT

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15210	45578	A	15300	710	1831	IRMKSKEIHARCIPYHSMARTQ PGTRNKENGPAIPTALDNNVASS DDTGRHRPQTITQLAPGFHPLQ LASFRMRVLFSLSGEGRSRGGPE LQFPASCRRRGEGSPGVRESGSG GIAATSTPNYPNPQDSKEHDIR GAEHQKQEQPAKPPHTARSAY PPQKSSYPANAKATRHSPETAA AKEARAPAAAQQRHQPNPSP APHTRPATAATRQPERRVPSPT HRHPAATRLSPRRQSPSPRPHH DRRGFPRLAETLQHPMCPLPLV ASAGHHRHHRLLLLAPQAPER EASDEIVFSGRSRSGCTEFQE SAMCFPNPGLPDSGESQAVTI LILRKFKQVIWVIEVPLDYKKG SWEYFSRMETHIMPFENIQSE
15211	45579	A	15301	77	1041	IPSCVVSIGIAAAF/HPGLASDAP ARASSWWTHVEMGPPDPILGV TEGFKRDTNSKKMNLGVSAAYR DHNGKPYSIHKAEEAIAAKNLD EDYLSIGRLAEFCKASAEVALG ENSEVSKSGREVTVTQISGTSAL RIRASFLQRFLKFSQDVFLPKPT WGSRTPIFRDTGMQLQGYRY DRKTCGDFDITDVEDISKTPAQ SLLLLHACSHNPTGVDPGPKQQ KEIATVVKKI/RLNLFALFDMA YQGFASGNGNKDAWAVRHSAN IRHCRCSQSYTKNMVVLHSEGVA GFTMVCKDADEAKRVESHKI LMCPMYSNPPLNGTRLLLPF
15212	45580	A	15302	1	1263	
15213	45581	A	15303	1	1146	MTGRQSLSPVLSSSLDSMSFT TRSFSTNYLFLGVSQVSNYGA RPASCMASVYAGAGSGSRISV SRSTSFRGGMGSGDLAAGMAG GLAGMGGIQNKETMQSLNDR LASYLDRVRSLETNKRKLESKI REHLEKKGLQVRDWSHYLKT EDLRVQIFANTVDNAGIVLQID NACLAADDPRVKSMTNVTWL PLETEMEALKEELLFMKKNHEE EVKGLQAQIASSELTVEIEKSTT VVTQTQTKVGDAEMTLTELRR TVQSLKMDLDSMRNLKASLEN SLREVEARYTLQMEQLNRILLH LESEMAQSRAEGHQIGEYEAAL LNIKVKLEASATYHRLDDDD FNLGDLDNSNSMQTI/QKTTT RRKVVSETNDTKVL

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15214	45582	A	15304	184	370	
15215	45583	A	15305	40	1411	RGDPRVRRRTQSLSPVLSLSPDS MSFTITRSIFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRRGGMGGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL ESKNPEHLEKKGPQVRDWSHY FKIIEDLRAQIFANTVEQCPTTV L/LRIDS\RLA\ADDFRVKYE\T EAGPCAQS\VENNIHGLCKVIDD TNVTRLQLETEIEALKEELLFM KKNHEEEVKGL*AQIASSELTV EVDAPKSQLAEIMADIRAQYD ELARKNREELDKYWSQQIEEST TVVTTQSAEVGAAETTLTELRR TVQSLIEDLDSMRNLKASLENS LREVEARYALQMEQLNGILLHL ESELAQTRAEGQRQAQVEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH
15216	45584	A	15306	392	1449	GPWEMLMTIKSHPD\AERQPOR VKKL\QVFWSSASLRER/GKTY LFWPKLKKA\AIPAAYREALDE ALGISGGGRDVGERVYKGPSM MANPQKPVLEALSSNKYLHLIC AKHCDRHEGYKDEIKVKEASS RVNGC\VEAMLSAPLPLDRRNE HVESKGKPFMTGLSPRVLSASR RDGLRERKGSFFRTVVLHDTKT DSNSDTE\TNSSTPPRTLLEMQIL SPTWTY\EISSRTLGCGPSVFQG RASYS\SPVSGPRLGCPLMDGGR MRCPPGNPESC\VEANLIPISVP VAPHAHQH\LVSVFWKITIVIG GKTCVAQNHSNEAKMKQRPEI NHASPPGAF\AWSQS\GEPIASAM TVPA

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15217	45585	A	15307	1	785	MWDVVGQDSSLLRGAGGPGQLQWFGRLQLHLGGLREHRDAWVHSRGLGSCSGMQGAATPTQNGRGCLSPAPASSMEHAAPAVPPCCSWCDSSSRSRWPATATTETGPRTPVPSAQESAVGLLTASLLKGDSGSTGFCPLLMSLAAPGTQQC SLGFCCTFERKRSVSPAAPGTAPELAAALMLMPRKNQIAVYELLFKQGMVAKEGVHLPRHPELADKNVPNLHIMKAMQSLKSQGHREEQFAWRHFYWHLTREGIQSIQ
15218	45586	A	15308	1	392	
15219	45587	A	15309	1	716	
15220	45588	A	15310	150	372	RRSNEWGVVPVVPARTGGG/HGQKTPPSPLPPSPSPSPPPPPA\APAKIPPLPLPLPPREAPPAPGPALP
15221	45589	A	15311	218	740	KSCPETVSRRKNVGSIKKHQGD KFNVPVCLKMTTKEFVLCGWVPCRCL/REGEEETVTTLDYSHCS\LEQVPKKEIFTFEKLTLEELYLDAQIEELPKQLFNCQSLHKLSLPDNDLTTLPASIANLNLREL DVSKNGIQEFPENIKNCKVLTIVEASVNPISKLPDGFSQLLNLQ
15222	45590	A	15312	96	297	
15223	45591	A	15313	469	5174	KMTSLAQQLQRLALPQSDASLLSRDEVASLLFDPKEAATIDRDTAFAIGCTGLEELLGIDPSFEQFEAPLFSQLAKTLERSVQTKAVNKQLDENISFLIHLSPYFLKPAQKCLEWLIHRFHIHLYNQDSLACVLPYHETRIJFVRVIQLLKINNSKHRWFVLLPVKQSGVPLAKGT LITHCYKDLGFMDFICSLVTKSVKVFAYEPGSSAQLRVLLAFYASTIVSALVAAEDVSDNIIAKLFPYIQKGLKSSL
15224	45592	A	15314	267	495	GCLL**CLCIRL/SKNRAERALRPYSDEALRLSSDPFRQRPKG GSGWSLLSVEINQYGYGRVMIGRSNSEVVVL

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15225	45593	A	15315	3	3027	AMEQAGTRPAATEHPRLRRPM PWLLLLPLLLLLLLLLPGPAASQ LRYSVPEEQAPGALVGNVARA LGLELRLRLGPGCLRNHLGAPSP RYLELDLTSGALFVNERIDREA LCEQRPCLLSLEVLAHNPVAV SAVEVEILDINDNSPRFPRPNYQ LQVSESAPGARFHIESAQDPD VGANSVQTYELSPSEHFELDLK PLQENSKVLELVLRKGLDREQA ALHHLVLTAVDGGIPARSGTAQ ISVRVLDTNDNS
15226	45594	A	15316	1	775	MPCVNGKYNSTIQAQLQMAQI LQDEGPYEVGIDEETGSQKGDG IIRSSRKLFTMALFLETNLLKD PLSRERRWRLELDGSGGREKG VAVFLRSAGIRQVQVAMEQAG TRP/AATEHPRLRRMPWLLL/L PLLLLLLLLLPGPAA/SQLRYSV PEEQAPGAL/VGNVARALGLEL RRLGPG/CLRNHLGAPSPRYLE/ LDLTSGALFVNERIDREACLSG AGANPVA/SAVEVEILDIN/DNS PRFPRPNYQLQVTRCWWTSW
15227	45595	A	15317	2	165	
15228	45596	A	15318	1239	2251	TCSSRRARRPRGRTVSQVRGPA PWAPRRARLQQRGSLRGAARS PASPTSA/PSYSRASASAGPAAL QPQGA VTPGPSANLAAPGGTL VPAEGPRMPVTAQSASSHPAP SASQPSPPAAASRGSLSPQEV ATLLASASSPTLDATRDAPATP RIAAPPGSATSSRGLGSAQGS LGTKEISIDSFGLGSPAVTQRTT APPDSAAALSQDTRPEAAGSWPG PQTGACSVGSGTDRRDTAAAT EAQHLSSESKEKTSAQKSGNCF GILKADFTISTLMDPEEMKDQF LRQVRLPSTDALKKQSI SNYRP PGKGPQYYLGDSA WNMVSA GTIEGFYKE
15229	45597	A	15319	46	2859	

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15230	45598	A	15320	240	924	NGEQKCILCHIVYSSKKRHSHE CRRCGPTEVSLSAYAKHISGQL HKDNVDAQEREDDGKEEEEE DYFDKELIQLIKQRKEQSRQEPS SSSQEVNSDDSSATFSVSFVYV WLKTILLTWPKEVKRLDTPGL ELWL.VPNMAELSEPEGVDWK ERCVALESQMKFRVQASKIRE LLAEKLLHNERLEYRDQRKDS ASFQRKKQFTYKASGIEMASDL SKAPLEIRG
15231	45599	A	15321	3	755	LRLPRSTRTRRGIVWRTGAAM GKVNVAKLRYMSRDDFRVLTA VEMGMKNHEIVPGSLIASIASL KHGGCNKVLREL VKHKLIAWE RTKTVOGYRLTNA GYDYLALK TLSSRQVVECVGINQMGVGVKE SYIYIVANEEGQQFALKLHRLR RTSFRNLKNKRDYHIHRHNVS WLYLSRLSGMKFCYMKQPCD EQGSQRLRIHMMGGQMWAAPIC QPRDLFVWFVLRAEACACCGA TSQORGALGVTSTCYRD
15232	45600	A	15322	1	1028	MNKTITTQEEVLPQADV VQRE EELNSLKQKLA AALLAEQEPQP ERLVSELQLPRKAAVFDQDEILR SSRQLVLPVLGVHRHVLVCC GGLRCLAGGLAAA SVGRGLG VDCDVVEMS NLAYQVLHGEAL AAQAKAASAAASLRGLNLAPP PAETVTNCADGGMLRVLTGVL GCLQPLKVLKIAASLGPSYSGS LLLFDA LRGHFCCIRLSRCLDC AACGKWPTVTTHLLDYEAFCGS SATDKCRSLQLLGPEDRVSVTD YKRLLDSGAPHLLDIRPKMEL PRKAAVFHDEILRSSQLVLP GVLRLHLLVGGCGGLRCLPAQY LAAAI VGRGLVA YDVV
15233	45601	A	15323	92	778	QGTTRRWSLGTCSLMTRTQFEV CTKVCVQESLQRPGEELKTRCP SVGAGYVNYGTPAHERJ/GAAV KTGREADKPEVTKTQFSTRK DE/TSLFGVPLQ*LLARHRAPP* RRT/RRLLEVARTPMLPAQASR SELAARQDSA WASPAAPASN/ RSVLRRCLLSARPPLCGPL/LRV LPSWRRQIIRENSAED* LHSEY RANRIRRRRGHPEN/WTKS*LE NPENLTRSSSAPAPC
15234	45602	A	15324	142	500	

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15235	45603	A	15325	3	343	
15236	45604	A	15326	1164	1648	PLMTPAPWPSCCCWRSLSSGRPL AGRQRLQPTSITTAANQPAPSR KKSTSRKKQRNLPAVSPAMVA VRRSCDLYRWSVLHYASQERR VRDAAKPESDIRKRTTTKTRR/ WRYIKELSRQPGVADMRQQP TQLVEVPWNEQTPEQRQTLQ RQHGRETRCSV
15237	45605	A	15327	28	417	
15238	45606	A	15328	2	440	
15239	45607	B	15329	1	441	
15240	45608	A	15330	22	584	IRGRVDPFSAVEPPPKMQIFVK LTGKTNILEVEPLGYG*KNVK AQASRDKVEGPPDQQRLLFAG KQLEDGRTLSDYNIQKIESTL/ HIFVRLRGGAKKRKKKSYTT/ PKKIKHKRKKG*SLAVLKYYK VDEANGKISRLRRECPSIDECG WGVYGVQVTFDRHYCGKCCLT LLFQOTRMTSNCMS
15241	45609	A	15331	3	954	LDARRHWEGTPEGFTHTSPDAW ADAGWKMAGEKVEKPDTEKE KPEAKKVDAGGKVKKNLKA KKPKKGKPHCSRNPVLLRGIG RYSRSAMYSRKAMYKARKYSA AKSKVEKKKKEKVLATVPKV GGDKNGGTRVVKLRKMPRY PTEDVPRKLLSHGKK/PFSQHV RKLRASITPGTILITGLRHGKR VVFLKQLASGLLLVTGRLVLR VPLRRTHQKFVIATFTKIDISN VKIPKHLTDAYFKKKLKRPRH QEGEIFDTEKEYEITEQRKIDQ KAVDSQLPKIAIPQLQGNLRS VFALTNGIYPHQLVF
15242	45610	A	15332	670	1008	WCILGVTPLMSRTALFLSRHT FFA/RHSHAASKL/EKKKKEKVL ATVTKPVGGDKNNGGTRVVKLR KMPRYYPTEDEVPRKLLSHGKK PFSQHVRLKLRPSITPGTILITG RHRG
15243	45611	A	15333	1	708	

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15244	45612	A	15334	1	1754	MRNEISDLTEELHQKEITIAITVT KKAALLEKQLKMELEIKEKML AKQKPWACLNVNAMP AIQVVFN LGRFRKCQDPHKAQEWVYPGY SGSDCEVFPEIMTSKNREEAMP EWKLWKKVVLSGATDAPSWD GPTFTDLNVFAGNMGLSDCTL LGKIWKIPGHFLHTSGPVSFHT KGLLNTPTKERWVGFGSEGR GVPEPGGCGVLAVPRRTPPSA AAMTGERLGRAWAGDRAAA SRSAVPVGTFGMMGWRPVAFG KNAKAYRGFGGIVTSLTPSCDK VTLLFVRILPGSGQSRDQSSPEK LTDTKSTSNKAYGFPECLRRPE STHIFFYDHLQLGSEQPRGTGT PLKWVSQKTLERETRQCQALVI WTD CDREGENIGFEIIVCKAV KPNLQVLRARFSEITPHAVRTA CENLTEPDQRVSDA VDV RQEL DLRIGAAFTRFQTLRLQRIFPEV LAEQLISYGSCQFPTLGFVVERF KAIQAFVPEIFHRIKVTDHKD GIVEFNWKR/LSTL*PHGLPSSL SVVCGVRSLSCRSVGF CWRSTP DPVCLCITSGGCRTASIAEQQL LPDPYSRFSIPEGQPP
15245	45613	A	15335	3	125	
15246	45614	A	15336	764	1005	
15247	45615	A	15337	1	3533	MELVNCVLMSTLGN TCCPMAL AMFRSSSLPRPGHSLTGSPLRV NLIHIFPLNDFHQNVVKINK DPPLGAAIGKESCPADNELHSL ERRPLSPKL VQALGVAGLSRPG PPHTGCAIWL LITDHKLLSEIL YDLLHQGLDILADPPDEGGIPR GKNLVELLQLPGLEEDKAFQKE IGLKILVFKAYSTLSSDGPPLFS ALRSLQGVQSSKVGESREEKSQ TEEEDPGNPWPQSLGASVSSS GKWGCLRTKP

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15248	45616	A	15338	1	2800	SISGPGQEAVPLRPKAEPEPGSG MVWDRQTKMEYEWKPDQGL QQILQLLKESQSPDITQRTVQQ KLEQLNQYPDFNNYLIFVLTKL KSEDEPTRSLSGILKNNVKAH FQNFPGVTDIFIKSECLNIGDS SPLIRATVIGILITTIASKGELQN WPDLLPKLCSLLDSEDYNTCEG AFGALQKICEDSAEILSDVDLD RPLNIMIPKFLQFFKHSSPKIRSH AVACVNFIIISRTQALMLHIDSF TENLFALA
15249	45617	A	15339	8	450	TWSWSPQAPSWARPSSQARAV SLLVARGQLCQGSRRRSGVGS VDAGAARTALRTLGTPLRRRP CGLGSHTKAAASGQDQGRGS RGRGSLGGRELGANEPLYQ/WR AHTLTVLFLTCTGLYVTLLEET PQDTAYNTKSEIAVVHLS
15250	45618	A	15340	246	559	MPVAVMAES/AFSEKLLDQCE NQLEAPGGIATPPVYGQLLAL YLLHN/GQRIWQRDFFGIYTTIN AHQWSETVQPIMEALRDARR RAFALVSQAYTSIIADDDFA
15251	45619	A	15341	129	915	RSQTQGRSAATAALNVIAGATP EQSGWGLAVRTVQRRGRPAK MPVAVMAESA/VSFKLLDQC ENQLEAPGGIATPKVYGQLL ALYLFHNDMNNARYL*KRIPPA IKSANSELGGIWSVGQRIWQR DFPWG/IYTTINGHQWSETVQPI IMEALRDATRETA/PLPVWSQA YTSIIAR*FCQPLLGLPV/EEAV KGILAEQGWQA/DSITTRNGSCP GKPVCRGPWDVFPFNKISLYS EPVAPVPPINQQLARLTDYV AFLEN
15252	45620	A	15342	1	529	MATLTISRAQTEADADYYCHRI KLVEGLDERTHKAYLSSSGK GCEFHMKVPGSPGLGPDILGSA QSALIQPPSVSGSPGQSVTISCT GTSSDVGSYDYVSWYQQHPGT VPKPMIYNVNTQPSRV/DRFSG SKSGNTASMTISGLQAEDEAD YYCCSYAGSYPPVFGGGTKLT
15253	45621	A	15343	399	737	WISGGNSCATT/LSDAGLSTTSN SIGSATVGARQAESASSQSGGGA LGRHCGASGKCAESLRREPVG ATNQWAPGWVVGPRASDSSHV VIGLGRSAWSPAEVTPSLIPGRG RTK

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15254	45622	A	15344	1	4320	
15255	45623	A	15345	1	966	MNVNLAEESEKGETVGEIKG GGIQMVMLASQPLTSYCAARFI TGHGQKLKSELKKTLLQVIMLNI QKVRIPTRDGYNEKDILSTGKN VEKLELSNIAGYPSNIEKKEYQE QSVLSCCSEKIDANPKSVVCSF FMQEQCTKGKRFILPGTSLVD RHLRYFGILPTVSNAAVVKEVP TVSNAAVVTEAPTGSNAAVVT EAPTGSNAARVMEVPTGSNA VVTEVPTGSNAAVVTEAPTGSN AAVVKEAPTGSNAARVMEVPT GSNAAVVKEAPTGSNAARVME VPTGSNAAVVKEVPTGSNA VKEVPT/GSNAAVVKEAPTGSN AARVMEVPTGSNAAVVKEAPT GSNAARVMEVPTGSNAAVVKE VPTGSNAAVVKEVPTGVTLRW SRKRPRE
15256	45624	A	15346	1	702	
15257	45625	B	15347	238	546	
15258	45626	A	15348	632	2361	FQSRFTLKNWNPGEQSQKII/CF QLGERAYQTDVLVKKVPRQSSV FSENQRMNNPERWFESTGCGK TYNQNRFAFNQHQRFHSGEKTY EHNECGKAFSWPSILSKHQRIH TGKLLYTCEDCGKSFVSHSYFI QHCKIHTREKPYECIKCGKAFS THSSYVQHLKIHTGEKHHECNQ CGKAFSHSSNLIHHQRIHSGEKP YKCKECGKAFNRQSNLIHQHRI HSGEKPYDCKECGKAFSTQLFL IQHQRIHTGEKPYECNECAKFS LNRTLTVHQRIHTGEKPYRCNE CGKSFQSCSQVIQHKRIHTGEK PYICNECGKSFGARLSLIHQHRI HTGEKPYGCREKPYECSECGK AFSQSFNLIHHQRTNNGEKSYE CNECDKAFSLSSLVQHQRHIN GDKPYECHKCGKAFSQGSHLIQ HQRSHIGEKPYECNECGKTFGQ ISTLIKHERTHNGEKPYECSDCG KAFSQSAHLIHHQRIHTGENPY ECSECGKAFNVCSLIQHHRHT GEKPYECSDCGKAFSQHSQFIQ HQRIHTGEKPYMCNECEKFSFA CLSLIQHKRIHTGEKPYVCAKC

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15259	45627	A	15349	3	354	EAFGGERVSSMSGLSGPPARR GPFPLALLLLFLLGPRVLAI HLPIINSRKCLREEIQQGPASDW RVRDLRPVWGRWRPAQ/RTSR S QILLAIFFSTPKRMQPRGNLPLTT EDYDMF
15260	45628	A	15350	283	393	YVYRRYGRFE*NDPSSALMST* GKRCQDCLDQRENKK
15261	45629	A	15351	1	351	
15262	45630	A	15352	1	867	
15263	45631	B	15353	1	1323	
15264	45632	A	15354	1	3669	
15265	45633	A	15355	362	1039	LESYLQPSAEGKTVSVFGETC ATPVGP/AAGPHTQ/LAQNIVTS WL.TGGRFIELKTVQILDRIELE KPCIDAEDCFNTEWSTFTLL KAWDEYLKAWFALHLEAMF QPSDSGKSFIFNMSVGYNLEGQ PLNPKNYPSQGVPRVLKSHRQD YLVGNKLSWADIHLVELFYVY EELDSSLISSFPLKPHTHVDNT KKGSHPHMCAITDYVNNPND RMPQREITFVS
15266	45634	A	15356	74	208	QRLTKLRETSRRLSSWQRSPSS TTSMHGAEWSPRWLLAAGV EFEEKFIKSAEDLDKVRNDGYL MFQQVPRLRLMG*SWSRV
15267	45635	A	15357	308	735	NQRCTWAYYSMTMEIFLISCVKI LSVRYAVQQLKTGVFCSLETQP SKMAPAKKGGKKKGHS/AIIE VVTQENTINIQQHIHEVGFKKC APRALKEIQKFAMKEMGTPVY LIDTRLNKAVWAKIRNVNTRI HLCISRKCNEDKE
15268	45636	A	15358	3	323	LSSLASMSFTTCSAFTNYWSPG SVQVPSYGTQPVSHAASVYAG LGGSGSRISVSHSPMAGGLAG MGGIQNEKETMQSLDRDLASY LDRVRGLETENWKLESKIQEH
15269	45637	B	15359	1	991	

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15270	45638	A	15360	40	1030	RGDPRVRRRTQSLSPVL.SLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL VESKIREHLEKKGPQVRDWSHY FKIHEDLRAQIFANTVDNARIVL QIDNARLAADDFRVKYETELA MRQSVENDIHGLRNVDDTN YHTDLQLETEIEALKKEELFMK KNHEEEVKGLQAQIASSGLTV EVDAPKISQDLAKIMAIDIRAQ YDELARKNREELDKYWSQOI EESTTVVTQSAEVGAAETTLT
15271	45639	A	15361	1	438	LHSDDL.SLQML.RCSPVATAASY TSGPGAPISSSFSRVGSSSFQGG LGGGFGGASGIGGITAVMVNQS LLRPLNLEVDPNIQARF/VHTQE KEQIKTF/NNKFASFDKVRFL EQNRMLEAKWSLLQQQKMAQ SNMDNMFQSYNNL
15272	45640	A	15362	176	1455	EIFPLVIQKSYKVSTSGPRAFSS RISYTSFGPGAPISSSFSRVGSSS FQGGGLGGGFGGASGIGGITAVM /VQVLHTQEKEQIKTF/NNKFAS FDKVRFLQEQNRMLEAKWSL LQQQKMAQSNMDNMFQSYIN NLRWQLETLGQEKLLKLEAELG NMQELVEDFKKKYHDEINKHT EMENEFVLEKDVDEAYKNKV ELESHEGLTDEINFLRQLHEEE IWELQSLSDTSVVLSSSHSLD MDNIITEVKAQYKEIANCSWAK ADSMYQIKYEDLQMLARKHGD NLRCTKTDIEMNQNVSWLQA EIKGLKGQRASLEATITDAEKR RELAIKDANTKLLLEAALQW AKQDMAQQLRVYQELMNVKL ALDIKTATYKKLLEGEESWQES RMQNMSIYSKTTSGYAGGLSS AYGGLTSPPLSYGLSS
15273	45641	B	15363	70	915	
15274	45642	C	15364	62	217	
15275	45643	B	15365	1	612	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
15276	45644	A	15366	3	841	STPKMPKGGKAKGKGVAPAPA VVKKQEAKKVNVNLFKEKRPKN FGIGQDIQPKRDLTRFVKWPRY IRLQRQRAILYKRLKVPPAINQF TQALDRQATATQLLKLAIKYRP ETKQEKQRL/LARA/EKKA AW PKGTFPTKRPPVLRAGVNTVT LVENKKAQLVVIADVDPIELV VFLPAL/CRKMGVPYCIK GKAS LGRIVHRKTCCTTAVTQVNSD KGVALAK/LVEAIRTNYNDRYD EIRRHWWGNNVLGPKSVARIK LEKAKAKELATKLGLNVHC
15277	45645	A	15367	2	1006	WINLKGNI LLRKRSLTSNFWPCK LRSRKRHTTRNLRLMNLWLSSH PPQSQNTKPPWCCQLSCSTSLLT LLGTSLPLLSYL IHLIPGPRQYP VIHRTSTLLQHISVGKEKFHKS QHWGFCNNVMMQLQLSPLK GLSLVDKVNRPALSGTRVLAS KTAWRJFQEP/SEPKTKAAAPG VEDEPLL RGNPCRFVIFPIEYHD IWQMYEKA EASFWTTEEVDLS KDIRHWESLKP EERYFISHVLVF FAASDGIINENLVERFSQIVQ/TE ARCFYGFQIAMIENIHSEMYSLLI DTYIKDPKEREFLFNAI/ETMPC VKKKADWALRWIGDK EATYG
15278	45646	A	15368	3	1368	QAQPMGRVGGMAQPMGRAGA PKPMGRAGSARRGRFGKCWSE GSPVHPVPAVL SWLLALLRCAS TMLSLRVPLAPITDPQQLQLSPL KGLSLVDKENTPPALSGTRVL ASKTARRIFQEPT EPKTKAAAP GVEDEPLLRENPRRFVIFPIEYH DIWQMYKKA EASFWTAEED LSKDIQHWESLKP EERYFISHVL AFFAASDGIVNENLVERFSQEV QITEA/RCFYGFQIAMIENIHSE YSLLDITYIKDPKEREFLFNAI/E TMPCVKKKADWALRWIGDK E ATYGERVVFAA AVEGIFSGSF ASIFWLKKGRLMPLTFSNELIS RDEGLHCDFA CLMFKHLVHKP SEERVREIINAVRIEQEFLTEAL PVKLIGMNCTLMKQYIEFVADR LMLELGFSKVFVRVENPFDFMEN ISLEGKTNFFEKRVGEYQRMGV MSSPTENSFTLDADF

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15279	45647	A	15369	2	621	RFIKMLSRHHQHVVHVLPLRLA PLPVAMEEEIPALFIDNGSGM/C KSSFA/GDNALRAIFPSIIGHPRH QGVVMVGMGQKDSYVGDQAQS KCGILTLKYPIKHGIVTNWDDM EKIWHHVFYNELCVALEEQVV LLTEAPLNPRANREKMTQIMFK TFNTQAMYVAIQAVLTLHSSGC TTGIVMDSGDGVTHTVPIYERH TLPHTLHLDL
15280	45648	B	15370	1	966	
15281	45649	A	15371	2	228	
15282	45650	B	15372	1	816	
15283	45651	A	15373	256	384	RKLLNEAPC*PMR*HSLLNRLA TSCNSWTVPVVPKFSKLRRGL
15284	45652	A	15374	145	375	KIAGKNRLNRNQCKERKVVQL WISEKKQREAVEDPSLDCCH KFPPGS*ERLHG*KRQWF*PP HTVEKQMRSCLL
15285	45653	A	15375	319	482	
15286	45654	A	15376	4776	5910	VCSTAGDVNGVCLLYDLHLHIA VASGSAGKECFARKPLL AEGV IYDCLQEFKEKKLVPA TPHAQV LSYEALLSAHD TIAQKDFEPLLP PLPDNIPESSEAMRIVCLVKNQ QPLGATIKRHEMTGDILVARIH GGLAERSGLLYAGDKLVEVNG VSVEGLDPEQVIHILAPRCLSP MSLADLPPLPREVLVLGAKLPV PSSSFLLPRED CQGPQPSLIT WFAPLETEPGVD RAMSRGTIMF KVVPVSDPPVNSQMVVYRA MTEYWPQEDPDIPCMDAGLPF QKGDILQIVDQNDALWWQARK ISDPATCAGLVPSNHLK/RIWT EPGICIFTKRLRCSGKQREFW SQPYQPHTCLKSTLCEYCNCP
15287	45655	A	15377	2	405	WSLVTRRALARVGLPG/SPPPRL LLLPLLLGWGLRVAAAASASS GAAAEDSSAMEELATEKEAEE HRQDSVSLLT FILLTLTILTWL FKHRRVRLHETGLAMIYGLEK ITIGVLDITGWPYCTIQPYNGFL
15288	45656	A	15378	1	3804	
15289	45657	A	15379	349	622	RPDVANLAFLARKEGTGRGFLS KKTAEASRWHEKWFALYQNV LFYFEGEQSCRPGMYLLEGCS GGTSPRSFRSSSRDSPISPLHPT AK
15290	45658	A	15380	314	483	

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15291	45659	A	15381	352	822	DPRRVQAFPAKMKFNPVTSDR SKNRKRHFNAPISHIRKIMSSP LSKELRQKYNVSRMPIRKDDDEV QVVRGHYKGGQIGKVQVYR KKYVYIYIERVQREKANGTTVHV GIHPSRVVITRLKLDK\DRKRIS DRKAKSRQVGKEKGKYKEETI EKMQE
15292	45660	B	15382	80	432	
15293	45661	A	15383	11	888	VKCRKAEGRRRESRLQTFEESQA VEAAMANVPWAECVCKFQAA LALSRVELHKNPEKEPYKSKYS ARANMIEVKALLGPAP\IEDED ERPEAEDGPGAG\DHAGLPAE VVEPEGPVAQANRLRL\AVNEF HLGVNHIDTEELSAGEEHLVKC LRLRRYRLSHDCISLCIAQQT WRCIGVRDPTTSSCAFLSTSTPT VHVSVKIQTPGLRPSNSTLVD DMESSFQTCFASPLSQDYVNGS NQEEIGTGVDRCIHKFLDIARQ NISFLQKRLQLSVQKPEQVINED VDVSELNRE
15294	45662	A	15384	1864	2705	WPGKVLAHRLHPWHRDPHGS GGGAGQELRRQGGCLEQLLYD AAHAQRLPPLDSVLPRAALPQD CQRASACEGDP\TLRPSHSPGH PRGAER/VPSTACIQRSWEGR/ WNRALQQVGGKSPWRGEYK EPRHPPPNQANYHQT/ACPAE R/CFRQGPQGGQLRRQQAEP SSLLSHQSPQSQTSLP*L*AR RSLGCGNPYLCPPWSQPLPETP AHQSGKQPSRSRNCSSWK*NYS STACPSHFLWRSRKFSTRASAST ASPCRM\TVRRTHQRFKARGTP
15295	45663	A	15385	1113	1378	RPHAESFVSGGIDPPGPGPGST GPGPL/ERQPCSLTSWPREPPSS SMKMLTQGP\SLTAPYKGTILGE VNPAHAISSARNTSSRTSV
15296	45664	A	15386	285	722	TPAHGVPVPGQSGRHRHW/QSA ARSLQGPSAW*PKTGS\LFATTW RCQTRASTCSAHWPLMAASPG AGGSSMASWR/DRP*PCPPPPAP HLPEAAFLR/CHDACP*NTGSA VPRGSCQPPAQQWDQGLAATR WGQAERLPRIYNWALAPP

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15297	45665	A	15387	207	605	FQASAEERFGTEDD/GSLRTRPPV MQSHQWPWRRPRPLVSRGRPQ TTPERHDSGGSPLTPRMESH EDEDLA/EGCRWP/EAGTVGV GPRAQGAQR/QAVLARKKHR RRPSKRRHWRPYLELSWA EKKQQRDERQS
15298	45666	A	15388	193	407	ACPKTSKNLRQRRLWNLA KHEF/SVDMTCGGCAEAVSRV LISLEVRVKYDIDLPNK/KVC IESEHSMDTLLATL
15299	45667	B	15389	321	625	
15300	45668	A	15390	275	690	SLWPPVIRG/SPKGNRPAIL TYHDVGLNMANKKSGDHP EREGTPRSFREVVSFAFG PGSSKLQIPKGSAPRCG VPGRGARRELQSFRA GPRRTQGSVPVGP RCQSRRLRS AQEEAKARHGG GLRAHRSF SWDIRMSSK KRFKFS
15301	45669	A	15391	2	137	PGRYRPN*LLSDASPGAG NEFQSTFLTPTILPSLRFP VLYTPNS
15302	45670	A	15392	1	648	MSLRKLTIMVEGKGGPN IPHACGCRQRSSIKVSL LPAVTSKSESPKEPE QLRKLFIGLSFETD ESLRSHFEQRRTLT DCAVMRDPNTKCS KGFVFVYATMEEKY HTVNGHSCEARKAL SKQEVASASSQR/ GRSGSGNFGGGH GGGGFNDNFGH GENFRGHSSFGG SHGGSGYGGSGD DYSGFNDGSNFG GGGGSYNDFGNY SNQSSNFGP
15303	45671	A	15393	1	3629	MTGICYTTEDE RSYKKNAPTA ASKKQKETQK FCLRV DGGQK VKL SVLQEK SAQLTV QLKSQ KFLGHPTAG RGRSEL CLDL PDP PEDPVALE TRSVGT WVRER DLGMP DGEA ALAAK VAVLE TQLK KALQEL QAAQ ARQAD PQP QAWPP DSP VRVDT VRV VEG PRE VEVV ASTA AGAP AQRA QSLE PYGT GLRAL AMP GPR PSP PV FERS QEV VETMCP VPA AAT SNV HMV KKIS ITERS CDGA AEMK WEDQ NIGD

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15304	45672	A	15394	1	1515	MGQVFRVVTGVGEQPGHPDQF PYIDSWLSIIQNHPKWLQACFET YCKTLMAQIKPGTIERDCKASV KEKDSQEKQKKPVLQAPPEELE SPALYAPIYPSLARLRQEAAAPA APRGSDSEESTPQATPCREEPEP LPEKETSSSYRSNAVHFLHNPT WADCKQLQLSFLNTEEHHRVI QAAFWLENNAPAGTGYIRQY AQQALPIEADTGWDPNQAQGL QSLQWYREALLNGIKAGGKKA TNIGKSVSEVCQKPDSESEFYER LCEAYQLYT*FDPEAAGNQCM VNVAFVSQAQGDIKRKLQKLE AKAVLRGKFIALNTYIKKAERA QTDILRSHLKKELKKQEQTSSKA SRRKDVTKIRAELEIETTTTKI QKINETKSWFFEKINTINRPLAR LTKKSRKELQITSLRKEMGDDTT TDTTEIQKIIQGYEHLVYAHKLE NLEEMNKFLEKYNAPSLNQEEL HTLNRPIRNSIEVVVIKKLPTKK/ SPGQDGFRAESYQIFKEALV
15305	45673	B	15395	1	1077	
15306	45674	A	15396	69	290	YYFDSPIHPLHLSGTLRPGGSRQ FPCDPQFLCRLHLTLASL*SLPG DLLRGLLHKLVCVRERLDLASL YAVGR
15307	45675	A	15397	62	201	
15308	45676	A	15398	3	429	LPSSVPRQPKMQARCLSRISIRA VEIYESDLEEGQGLLHEFSQFVL DRPPPTQSRYAQELVHTCYLHT LASL*SLPGDLQRGLLHKLVCVR AERLDLASHHAAVGRSEFFW TPYTHSPPGAGVGHPPWHTRL PWGVPAEGHQ
15309	45677	A	15399	303	612	PSSSIPVYHCSLRGICIPVLGLKR AANVGVSLEASPLLSTPGGLGI CLSCGGTRTVGSRVGSIFPW*G EGTTGITGSISCKGSSDVGSNRT SGVDFPRRVE
15310	45678	A	15400	1	273	

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15311	45679	A	15401	1	406	MEEGWIRLPDGRVAAPQLLGA AVVLAVQETTHRQESLEKLL GRYFYISPLSAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWVVLGLTDFKN EATDPPGVKLQTFVSVTTHKG SVDPNSEKQDQLLQRAKEQSFH SVEGDPSRDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVVKRKTLPANTQTA SPRALADSLMQLARQVSR*RAI SCCPSH*LPSAKCISVSGIGGFL VSLTSRMKPRTLLE
15312	45680	B	15402	1	930	
15313	45681	A	15403	391	617	LQLQPTG/CNFLYFYVGYMKIL GFCFHIVEERGGLWYPCFYC NLSSLGG*RSCSHTRIVPSLLMP KLGPGGQVC
15314	45682	A	15404	1	1860	
15315	45683	A	15405	1	531	
15316	45684	A	15406	2302	2691	
15317	45685	A	15407	520	2883	
15318	45686	A	15408	3690	4727	ENCHWGCHEPCDIGSSIISPLA YWEQYHRVTYISRDTGESSIVFP ALVTMLRNLFILAGSSDPHFHT PMYFFLSNLSWADIGFTSATVP KMIVDMQSHSRVISYAGCLTQ MSFFVLFIACIEDMLLTLMAYDR FVAICRPLHYVPVIVNPHLCVFFV LVSFLLSLLDSQLHSWIVLQFTF FKNVEISNFVCDPSQLLNLACS DSVINSIFIYLDSIMFGFLPSIGIL LSYANNVPSILRISSDRKSKAF STCGSHLAVVCLFYGTGIGVYL TSAIVSPPPRNGVMASVMYAV VTPMLNLFYISLRNRDIQSALRR LLSRTVESHDLLSQDLLHPFSC VGEKGQPH
15319	45687	B	15409	1	3195	
15320	45688	B	15410	1	1819	

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15321	45689	A	15411	399	1089	LLTPRTDLQEMPLDNAIEIWEYWT DGSYLRGEVFQWYDHLALIFVP QTGIEDVIWHIEALPNYIQKVCE RRNPYNQILSLQCAQHEIFLVS WKLVCQKQLEGDDMLVGTTA SNLLLESEQSTSNLNEKINHLEY EDQYKDNFEGEGNDGGILEDK LISN/NMGGPDSPDSVPVE/P/M PTMTDQTTLPVNEEEAFALPEI DITVKETNAKRKRKLIVDSVKN LDSKTIRAQLNDY
15322	45690	A	15412	3	809	FKDDDDMLVSTTTSNLLLESEQS TSNLEKINHLEYEDQYKVDNF GEGNDGGILDDKLISNNDGGIF DDPPALSEAGVMLPEQPAHDD MDEDDNVSMGGPDSPDSVDPV EPMPTMTDQTTLPVNEEEAFAL EPIDITVKETNAKRKRKLIVDSV KELDSKTIRAHLSDYSDIGTTLD LAPPTKKLMMWKETGGVQKLF SLPAQPLWNNRLLKLFTRCLTP LVPQDLIKRRKGGEADNLDEFL KEFEHPVFPREDQQQ*HQQRD VIDEPII
15323	45691	A	15413	1	595	MVNRSHFRGVGPECHQQNSHG HLNSITETSNSTLRAAPLQPTR DPSDMAVFEIDELPEGA VKPPA NKYPIFFFGTHETAFLGPKDLFP YKEYKDKFGKSNKRKGFNEGL WEIENNPGVKFTGYQAIQQQS SSETE GEGGNTADASSEE EGD VEEDGKGKRKNEKAGSKRKKS YTSKVTKKLLIVINVICISIKHF
15324	45692	A	15414	41	785	GKGWAGGASGPANHGPAAGG RSPGMLRGDQGLPGRGAAGM ARPRSREYKAGDLVFAKMKG YPHWPARIDELPEASVKPPTNK YPIFFFWHPMKPAFLGPQDLFP Y*EYRGKFGKSNKRKGFNEGL WEIENNPGS/IRFTGYQAIIQQQ SSFRTEGEGGNTADASSEE EGD RVERDGKGKVRKNEKAGSKRK KSYTSKSSKQS/RKSPGDEDA/D KDCKEEENKSSSEGGDAG/NDT RNTTSDLOKTSEGT

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15325	45693	A	15415	1	1272	MWSGAGPGLAVWPQLVTVLSL SLSRNLCKWGLSFLACLLGSD MADAAMQHYGVNGYSLHAM NSLSAMYNLHQQAQQQAQHA PDYRPSVIALTLAERLADIILEA RYGSQHRKQRRSRTAFTAQQL EALEKTFQKTHYPDVVMRERL AMCTNLPEARVQVWFKNRRA KFRKKQRSLEQLQKQKEAE GSHGEGKAEAPTDQTDTEQP PRLPGSDPPAELHLSLEQSASE SAPEDQPDREEDPRAGAEDPKA EKSPGADSKGLGCKRGSPKADS PGSLTITPVAPGGGLLGPSSHSYS SSPL/SPLPSAGAIPPAHGGHQQ PGALLVLRSGSGPCCSGGCC CALPGRQHGPAGLTA/SASPTTS PCQQPLLP/SQGVWGSPLLPA AGLAPASATLNSKTTSIENLRRL AKQHAASLGLDTLPN
15326	45694	A	15416	1	1152	
15327	45695	A	15417	8	82	
15328	45696	A	15418	1	1350	MGSEKDSSEPRSTSLHAAAPDP KCRSGGRRRLTLHSVFSASAR GRRARAKPQAEPPPPAAQPPPA PAPAAAQGPPEALPAEPAAEA EAEAAAAAEPGFDEEAAEG GGPGAEEVECPCLVRLPPERA PRLLSCPHRSCRDCLRHLYLRLEI SESVPISCPECSERLNPHDIRLL LADPPLMHKYEEMLRRLYLAS DPDCRWCPAPDCGYAVIAYGC ASCPKLTCEREGCQTEFCYHCK QIWHPNQTCDMARQORAQTLR VRTKHTSGLSYGQESGPADDIK PCPRCAYIHKMNDGSCNHMTC AVCGCEFCWLCMKEISDLHYL SPSGCTFWGKKPWSRKKKILW QLGLTGIAPVIGISLIAGIAPAM VIGIPVYVGRNIHSRYDGKEN/S KHKRNLAITGGVTLVSIASPVIA AVSVIGVPIMLAYVYGVVPI SLCRGGGCGS
15329	45697	A	15419	2	540	

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15330	45698	A	15420	1	530	SRTTPGKAPKETWGDQAGSGK GGQGPTRKIPRRTSSHLPPSPA AGDCPLATPESPPLAPETPDE AASVAADSDVQVPAGPAASPKP LGRLRPPRESKVTRRLPGARPD AGDGDHLSAVAERP KVS LHF D TETDGVYFSDGEMSDSDVEAED GGVQRGPREGAKEVVRMGV LAS
15331	45699	A	15421	1	2989	MLLVMYWAPAPPPVHMSQFLT TGPKCLELSLDHGRDSQEITAS GLLWLQHAACGLAQWNQKPH PPFLTLLQAEPPFERARSCDIYIR IKMLQTAQQHQVGLAPTERKE ALRGSPQKSASGQRPGSLDR ELLMLIKISKCLRVSPGSSVLG TESTGPVPGELVLCQQDAGATQ EGVCYGRELMICRCDSPRLME PWGVKGTPVFRTDLITAMKIP DSYQLSPDDYYILADPWRQEW EKG VQVPAGAEAIPE
15332	45700	A	15422	218	404	
15333	45701	A	15423	1	422	
15334	45702	A	15424	160	470	LTMLFAACVFSGDEIMASEERQ PMEEEWSRSSTISGEDGERWTP DTAGKAAQGIAGDVVWVSPLP PSKVSAASKPPKS/HHPFFKWH NFSNLMKMFYKMYFSKN
15335	45703	A	15425	21	375	TFENTRFWDVQIPVPTGERRNE WALPPPGAGSVPAGGWSRPLTP GRCDSQGRGRSRRAPLSRSPL PPLRRSPTLPGEPHPAHRPLRVH PRHGPRPSHLACLNSQAPDASR LRASANQ
15336	45704	A	15426	155	340	

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15337	45705	A	15427	1	2658	MIINTIITTTTITITITIMSSSPIT ITNITIIQHHHHHNDQRPSLGK CRGLYIRVRKVPGERATANSRC PINAQGIESCWNGVMALWLG NSTCSRLPELTSEDQPADSP GDEDPKPWWDPHEAPLTGYF HPYGAAAFVPRHAGNFKDRREV PHQDTSFCSAQGFWILPSACKT GRVALTLTLIGAYQTLTEADV KGLTAARAASPGAKWRTQFPC PAGTCSSQAGNGQLEDCLPYPP GPSAPVGSLSRSSANGEFIIGRVI KAMNNSWHPECFRCDLCEVLE ADIGFVKNAGRHLRCRPNRE KARGLGKYICQKCHAIIDEQPLI FKNDPYHPDHFNACANGIKLG VFLTRKDLTADAEKLGELY CLPCHDKMGVPCGACRRPIEG RVVNAMEGKQWHVEHFVCAKC EKPFLGHRHYERKGLAYCETH YNQLFGDVCFHCNRVIEGDDE GDGFAHRYSPYDSCEVDQSPLE GQQLKSIRKPLAQSQPLPTPV MLHPGCKTQIREAPGSAALLESV RRRPRPGLVPEEESAAVEAV RHHHLQNFSLLETLNGQKLG GHFCDVTVCHEASLRAHRCGL AIGSPSFQDKLLGPSEIRVPSV VPVQTVRQLVELLYSGSLVVA QSEAPQVLMAASVLRIDSYRR MHADYRTRSSAPASTSAPALP TPVPPPLAPEQLRHRLRHLLAA
15338	45706	A	15428	708	892	
15339	45707	A	15429	2	713	
15340	45708	A	15430	212	1246	DLPLAVHGVQSDSGAQAVASR SGDESSIVCLKEESTVNMTRFCS LPLAVISVSTAKCQVKSFEII GRVIKAMNNSWHPECSAVTSA RKFWQILHLSRMLVDRKDLTA DAQELKGELYCLPCHDKMGVP ICGACRRPIEGRVVNAMEGKQW HVEREQYMDPGILSALIDPKYL LILSHRGLHMKSMKGFYFAKL YYEAKEDYLAKKYICTYINVQE RDPKAHRFLGLLYELEENTEKA VECYRRSVELNPTQKDLVLKIA ELLCKNDVTDGRAKYWVERA AKLFPGPSAIYKLN/DGWVRG QMVPKPDDEGVQVRGRSGRPD AGWRLNRRSSVGGSAWRLRPQ

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15341	45709	A	15431	129	444	WGGPGRQPDGGRVPGRCGPRR PATWESPAACRPRQSRHHSFE *GGSRSGSHKRPCSPSPAVLRA RDQVVLHTSFATEGDSSEDR STPLARRCLCSHRSGEA
15342	45710	A	15432	1	2446	METSLMVQVCGGRDCNALLPG NLCSQPTQVPLEVDGDDGPG GLPLNAAAPPSSVPPVPSEALPP PACPSAPAPWRSIISRLFTGSPA AEAAHPPPGGALDFGALRTSSC LSQSHGHIPGGPGLGLGAVRVP VPSEEDPASLFTEVPAAEAPAT VQSVEDFVANDRLDRSFLEDM TPARDEKKVGAKAAQDSDTG RASRAPEQQIPHGGHWRGHSRS YERFRPPDMVSAGPGPSDGEAL GGNPVAVGFQDDVDLEDQPRGS PPPPAGPVPSQDITLSSEEAEV ADPPKGPAPAPQCCEPETKWS SIPASKPQRGTAPMTAAASPPWP GGASVHTGLEKCSSTRPPAEIEP GKGEQASSESDPEGPIAAQML SFVMDDPDFESEASDTQCRAVR RVLPAQRAENAYGSAFQPGAL KPECRPTLKGPGPVPSKAGKK TEATSPRPTGGASPLAHGATVG AAWGLGMASWPIGSSLAPTRA RTREPRQLQRRVGSELPGDPCSG SGASCRQVCARGRATSVRLPAL ESLWPLSSDGSAAAREGLEGPR LRQAAAPGGPGPPLPLSRPPSP ARRMRGGAAGVAGRGAAAPLE GRVRLGVGFLAETAVRAGAGA LAAADAPGSRTPRARPLVAAAG SGAAGGRCPVPSRRQREAPSPL GGAGVDLQLECLTSEKAGVGA ATGGVLEALARAIRQKKEIEIQ

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15343	45711	A	15433	26	963	FMIWAGQNRKVKQDFVIQLRML TPVVPVPPQAAFPNAQQPRAAASA PQTRVRAPRWPLGNVVVLGTE DAAGPSRPASEPPASPALPGPAL ELGLPNHPKQT/IRPRLAPRRSH PKDSCITIFKLSFLKNKIFNNSV GDQVNLDYKLISGTEYDILNFW NFRILAKTGCSKDGHRNPRSRP TQEEGSGKPKKSLVKERSGAQE DLVPVPPEEKLELSGTSMGPCCFS KTSYGPHIYILSYKGTATAG HRWPAAYAPLNCVPPPETTM PVSDLGSLPHWASRIATPPSMW LCCLAAALRVLAYSNSSAEYV SQS
15344	45712	A	15434	803	1305	RSKPCRSHNVFSWVAHSRPC CPWSGYSSRLCCLSCCITLGPY QLKNRQQRNGSYKSGNYLCV GNRLLFWVWIFQKGGRS/WLP RSDWVTSYKVMVSNDSHTWV TVKNGSGDMIFEGNSEKEIPVL NELPVPVMVARYIRINPQSWFDN GSICMRMEILGCPLPGWEH
15345	45713	A	15435	2	377	ARELLKAVWRPHKVAVMHCR GHQRASTLVGLGNSRADSEAR KAPSAPFRASVTAPLLPQAPDL VPTYSKKEENDFLQAKGGQVME EG*IRLPDGRVAADVLAHVHETT HRGQELLEKLKGWYFYISH
15346	45714	A	15436	77	679	KMKTNQMGKLSKVVEMNATIS EIRLINNRKDVVEYQQEILQLEAV WKLHKVAVMHCKGHQRASTL VGLGNSRTDSESPKAAASAPLRA SVTAPLLPQAPDLVPTYSKKEE DFLQVEGGQVMEEGCIRLLDG RVAVPQLLGAAILVAVHETTHL RS/ESSLGKLLGQLFSTISHFVSL CQNLTQRCVTCRQHNAHQGPA VPPGMQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15347	45715	A	15437	2	881	HARCTGIAARAGLLDPRHTGEA LAARSRIDLARRPHWPRGCGTG GGGGGCAGLGGAWLRGNDVA VPARALVTAAPASSMSPPIPA AARPVSSSIPAASPSPRCGLRAG PAELRCPRRLRQARAEEPPRAG PAPGRRRPTPGICAPLSPLRLA GGTAPSLPGVTRGSRVGRRLRP SLGGAGCRVGRKPRLLPPGRR CSTGLPPPAGTGAPAGVCWED GDPGHLEAAALLRRLGGQIRAL AGHRTAGWAQHGLSPREAVRP APAARGTLLRRSNSRRHLQNP ANFGGTAT
15348	45716	A	15438	3	502	GRRDSCLPVVVAPRACLHPRG QVPRLGSVGKMATPGMSWQQ HYYGSAAKFAPSATAQLAG HSMDSQEMHLKMSKKIAQLT KVYIALNTKNDHEHSAIQALKD AHEEEIQHILAETREKNLQYKS KVTEELDRLRRKIQVLESSLEDHI KMKQALTEFEAYKHR
15349	45717	A	15439	29	230	LQIDCKNKPAILRGPTDPLKEA DCYCRTWERPQILLPKWEGTR KPILVI*QNKAHQHAQITLLHQ
15350	45718	A	15440	73	335	FFWGGIEEPCFVILSGSVFWFL JWVGASASPVVGDVFGRGGSPP PTSTVGAFITVLWGVSVWLKRV CGSSWDC*FVLAINLELKFTM
15351	45719	A	15441	373	513	
15352	45720	A	15442	1585	1649	KNSNIQHSFKITLVHQWFQTK KKFLIYLKKNSSGLVDP*MVHT TRLCADNPQYQPRARKSHS*VK GESTTLREHPMGQKNLNSLQP
15353	45721	B	15443	1	696	
15354	45722	B	15444	49	525	
15355	45723	A	15445	113	474	SIPYKNKEEEEGKGGEYYIKGT CHGTGKGSEQQPSALDLPDRAY PNEKEPEN*W*LI*QNKAL*HS PKNHTSSP/RNGSKPRKKSILNL KKNSGG*LLS*LGRHQKVKPN ARKSKNQYKK
15356	45724	A	15446	47	614	TGCPRCQKQNSTCIAAVKMEGPI SVFGDRSTGETIRSQNDVTITN DGATILKLLVEHPAAKVLCEL ADLQDKVEVDGTTSVVIAAEL LKNADELVKQKIHTPSVISGYR LACKEAVFYLTENLIVNTDELG RDCLINAAKTSMSSDIIGINGDF FAN/MVVDVAVLAIHARRGQ/P RYPVTLLY*SHGES

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15357	45725	B	15447	707	1826	
15358	45726	A	15448	108	397	
15359	45727	A	15449	1726	2464	SKAVQLEAGGLQLFCCKMAP DPNITDVFGR TALHYAVYNEDT SMIEKLLSYGANIEECSEDEYPP LFLA VSQRKVKMVEFLKKKA NINAVDYLGRSALIHAVTLGEK DIVILLQHNIDVFSRDVYGKL AEDYASEAKNRVIFELIYEYER KKHEELSINSNPVSSQKQPAK ATSGKEDSISNIA TEIKDGQKSG TVSSQKQPAKDOTSDKNDVSN TATEIKDEQKSGTVSSQKQPAL KDOTSDKNDVSN TATEIKDEQK SGTSVFSETTGLEGYK
15360	45728	A	15450	2	675	
15361	45729	A	15451	1	467	DHSSSPAREQNWMEFDEL EVGFRRWVITNSSELKHHVLTQ CKEAKNLEKRLGELLTRITSL KNINDLMELKNTARELHEAYTS INSWINQAEERLSEIEDQLNEIK REDKITEKMKNSTTVRVAAASM QSKLLQGVAAEEGPLRLTRSAF
15362	45730	A	15452	2	632	
15363	45731	B	15453	355	894	
15364	45732	B	15454	99	716	
15365	45733	A	15455	1	1140	
15366	45734	A	15456	1	1476	MEVNREKQLENELEVIGSEEQNL EEEGLMIGGVA VRLVPDDIVIP GGVNATNGTEARDALRVKVA MSVTLLSGIIQYLLSALGWSYY TVDGVSQKNPRALGVTADQLH AIFTTMSDEQASFRGFVAIYLT EPLVRGFTTAAAVHVFTSMKL YLFVGKTKRYSGIFSVVYSTVA VLQNVKNLNVCSLGVGLMVFG LLLGKKEFNRFKEKLPAPIPLE FFADHNSSPAREQKWMENEF EWTVEVSFRRWVITNSSELKEHI LTQCKEAKNLEKRLLELLTRITS LEKNINDLMELKNTAQEFHEA YTSINS/RNQTEERVSEIEDQLN EI*CKDKIR/EKKRMKRNEQSLQ EIWDCVKRPNRLTGVPESDGE NGTKLENTLQDIIQENFHNLAR QANSQIQEIQRTPQRYSSRATP RHIIIRFTK VEMKEKMLRAARE KGRVTHKGNPIRLIADLSADTL QARRQWEPFINILKENFQTRISH
15367	45735	A	15457	1	1185	
15368	45736	A	15458	1	2367	

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15369	45737	A	15459	1	744	
15370	45738	B	15460	337	1515	
15371	45739	A	15461	1	1197	
15372	45740	A	15462	1	714	
15373	45741	A	15463	142	601	HQRTKVYKFTKMRKNQPKKPE NSK/TQNPPSPSKDHNSLPAREE NWMENEFDKLTEVGFRRVWIT NSSELKEHVLTCCKEAKNPD RLEKLLTRIISLEKNINDLVELK NTA*ELLEAYTNINSQIDQVEEK I/S/SIEDQLNEIKLEDEIREKKKK
15374	45742	A	15464	153	474	OTKSNVNIKKQDVHTKTPSEG HQHQRPKADHNSLPAREQNWIE NEFDELTEVGFRRVWITNSSEL KEHVLTCCKEAKNLEKRLQEL LTRITSEKNINDLMELKNTA
15375	45743	A	15465	1	2172	
15376	45744	A	15466	1	1640	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRTRLRAEDVFPPI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNPDQGT SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPLDI IPSCALAHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGITINVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEFDHLPAGNC YVVRNEDCIGFSGFYNVISL GVYLVEQQKGWEDTHSKTPSK GHQHRKSKVDKSTKMRKNWS KNAENSKNQNALSPNDRNSSP ARAQNWMEKFDKLTVEVGR RQVITNTSELKEHILTQSKEAKN LDKRLQELLTRITSEKNINDL MELKNTARELREAFVFCVNCE AVSLITSLREDSHWLEDKSGHR M/RRHQE*KCEYFHPPHGLQF YQLPESDSSHDPWPHGGSFSL
15377	45745	B	15467	50	1603	

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15378	45746	A	15468	528	1413	QTERNSTSTSKTPSEGHQHQRPKVDKSTKMGRNQCKKA*NSK SQNACPPKDHSSLPAREQWTW MENEFDDELTEVGFRRWVITNSS KLKEIIVLTQCKEAKNLEKRLE ELLTRITNLEKNINDLMELKNT ARELREAYTSINSRIDQAKERM SEIVDQLNERNDRENGTKLENT LQDITQDNFPYLARQVNIQIET QRMPQRYYSRRVTPRHIIVRFA KVMEMKEKMLRAAREKDTSVK QKVNKDIQELNSALHQVDLIAI YRTLHPKSTEYTFPSAPHHTYS KTDHIVHSILCDGS
15379	45747	A	15469	368	679	SSQLNKAPSLFNPVSEEFCLWL LLLQKELLTRITSLKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK
15380	45748	A	15470	865	2055	QTERNSININKKDNIAKTPSKG HQQQRPKVDKSTKMGRNQHK KA*KFPKPGMPSPPK/DHNCSP ARE/QNW/MENEFNEFDLTGA GFRRWVITNSSSELKEHVVTQCK EAKNLEKRL/QELLTRITSLKNT INDLMEKQDITQENFMKHTQ VSIAQADQGRKERVSEIEDPTL MDIKCEDKIREKK/IKKRNEQSL QEIWGYVVKRPNRLISVPESDG ENGNK*ENILQDIQENF/FPNL TRQANIQIETQRTLQRYPLRR ATPRHIIIRFTKVMEMKMLRA AREKGRVTHGKPIRLTENLSA ETL*ARRE**PILNILEKRNFPQR ISYRAKLSFISK/GKREIKSFIDK QILRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKLKRLPT
15381	45749	A	15471	1	315	
15382	45750	A	15472	1	2775	
15383	45751	A	15473	1	1017	
15384	45752	B	15474	1	3105	

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15385	45753	A	15475	1	1115	MKWL LLLGLValsecIMYKVP LIRKKSRLRRLSERGLLKDFLK KHNLNPARKYFPQWEAPTLVD EQPLENYLDMYFGTIGIGTPA QDFTVVFDTGSSNLWVPSVYCS SLACTNHNRFNPEDSSTYQSTS ETVSITYGTGSMTGILGYDTVQ SGYHHGNHRLNLKGLCSSKRSS TTPPLYDLGQVAPPSGVS SSC DDQSGSVVIFGGYSSYYTGGL NWWPVTVEGYWQITVDSITMN GEA\IACAEGCQA\VEPGTFFVT GP\TSPIA\NIQSDIEA\SEELDG\D SVLICSAISS\LPDI\VFIT\NGVQY PVPPSA\YILQSEGSCISGFQGM NLPTSEELWILGDVFH\PASTLT VF\DRANNQVGLAPVA
15386	45754	A	15476	1	765	
15387	45755	A	15477	470	479	PRNPSSFLQVQVQHRFLQLFVP FHFVFFLASLYVMVTLTTWFR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT
15388	45756	A	15478	1	896	CLPFGGPKPNPWDKDGCGQR PQPRHLPGPGTAAQRRQCPSE KSL\CRWPSTATSCSLFYIL LHV GAS/CNLLPPAVKDSGKG VGQDTQVLSGSGAVYRVCA GT ATFHLLQAVLLVHLHSPSPRA QLHNSFWLLKLLFLLGLCAIAF CIPDEHLFPAWHYIGICGGAFAI LLQLVLITAFHNSWNKNCNEAS YLAEVFGPLWVVKVYSYEFQKP SLCFCPCPETVEADKGQRGGA RPADQETPPAPPVQVQHLFLQL FCLPLRLLPWLTLCHGYPPYQLV QASAGCGCKPFAPYSL

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15389	45757	A	15479	1	1016	MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARI VFIRIARPRDGSFAYESVPWQQS ATQPAGLSVVTTVWGVGNAT QSQVLGNPMGPAGSPSGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQGVYSRGGYP GAPGFTTGYAGGPGGLGLPSH AARPTDFTQAAAAA ATATATAT/GHRGCSGAE AEPDAGAMGAGQSFNSQFLQHG GPRGPSVPAGMNPTGIGGVMG PSGLSPLAMNPTRAAGMTPLY AGQRLPQHGYPPQAQPLPRQ GVKRTYSEVYPGQQYLQAYP VHSGLSQFPTWQETPRHP
15390	45758	C	15480	1	585	
15391	45759	B	15481	1	885	
15392	45760	A	15482	3	440	GPWPRPVAYLSKQLYRVSKGW PPGLRALAEMALLAQEADKLT LRQNPNI/IGPHAVVTLMTTKG HH*FTNARLTYVKIPT*PLKF/G NTLNPITLLPVSESPVEHNCVD VLDSVYSSRPNLRDHP*TSVDC ERYVDRSSFTNRCKVTR
15393	45761	A	15483	3	368	
15394	45762	C	15484	109	276	
15395	45763	A	15485	1	1710	
15396	45764	A	15486	221	784	QNSLRSMCQKEKKMAAGVLT HTC/GPWPRPVAYLSKQLDRIS KGWPPGLRALAATALLAQEAD KLTLGKT*IRPPHAVVTLMTNT KGHHWLTNARLTKYQSLCEN PHITTEVCNTLNPITLLVSESL VEHNCVEVLDSVYSSRLNLRD HP*TSVDW*LVHDGSSFTNPCK VTLLKMTSAAPVTPRS
15397	45765	B	15487	509	661	

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15398	45766	A	15488	1370	2243	LGKLRLESCGLVAAVRPHSGGL AMPLPNATRPASGRSED/AELK LALHGHRSLSLQGRKHRGVH DNSDIPQAALVGGTTMIIGHVL PDKETSLVDAYEKCRGLADPK VCCDYALHVGITWWAPKVKA EMETLVREKGVNSFQMFMTYK DLYMLRDSELYQVLHACKDIG AIARVHAENGELVAEGAKEAL DLGITGPEGIEISRPELEAEATH RVITIANRTHCPIYLVNVSSISA GDVIAAAKMQGKVVLAEETTA HATLTGLHYHHQDWSHAAAY VTVPLRLGIPPH
15399	45767	A	15489	307	600	VSRRASSGSPVPLGSLHLQHS PA/PSAAPKPRSPPARLSRPHLR GESAAPSLSPGPASLAAAAA RVPAQSPAPSTTPAPRTTLAPR VPHRLAPAP
15400	45768	A	15490	3	222	
15401	45769	B	15491	1	1131	
15402	45770	A	15492	136	201	
15403	45771	A	15493	3	556	ELPRRLVCSKLRADPGRLT CARPGMSRYLLPLSALGT VAGAAVLLKDYVTGGACPSKAT IPGKTIVITGANTGIGKQTALE ELARRGGNIILACRDMKECEAA KIDIRGETLNHHVNNARHLDSL SKSIREFAAKIIEEERVDILINN AGVMRCPHWTTEDFEMQFGVN HLGHFLTTWC
15404	45772	A	15494	11	559	
15405	45773	A	15495	1	312	MAPAADREGYWGPTTSLDW CEENYSVTWYIAEFVWLMGSG FLPTPSSRLDTASRWVRS LPPSRSPAGRQPGPAEELPKAS PCPWGKLSLRPFASFSSSGPS

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15406	45774	A	15496	2	1605	WQLPHPPAAPSAARQILRACQLS SVTAVAQSCLYGKQLC/GLTTG NIAGAGLLFFGGGIGGTILYAK WASHFRERVEKTIPYSDKLFV VLGSAPYNVPLPKKSTQSGPLK ISSVSEVTKEFKQPASQLQKQK GDTPASATAGDTVLVPGVQHE ESLKTDPAPIDEKGKPTALSEEA SSSSIRERPCEEIAACLAQEEKQ EQVKTESLAKSFEDALRQTANV TLQAIAAQNTVVQAVNAHSNII KAAMDNSEIEGKKKSAKWHTV QGALKEHRKAVDEAANALLKA KEEVQAAQFESKLVSQYHEL GQAQDDFKRQLDSITPEVLPGW KGMSVSDPADKISTDDLNSLIA RAHRHIDQLNRELAQEKATEK QHITLALQKTLQEKVQEQELK YEFQNLSEKLSEQLQFHHL SEQVHNFTLDINTAYARLQIE HAVQSHAVAEERKAYQLW LSVEALKYSMTSSAEMPAVPL GSAVEAIKANCSDNEFTKALAT AIPPESLTHGVSEETLRVRFYA VQKLARRVAMID

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method in US 59/540,217	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
15407	45775	A	15497	89	2490	PKCCFFCLLSGETAAQSCLCG KVVLRLPLRCRRYSTSGSSGLT TGKIAGAGLLFVGGGIGGTILY AKWDSHFRESVEKTIPYSDKLF EMVLGPAAYNVPLPKKSIQSGP L*ISSVSEVMKESNRPAQQLQK QK/GDTPASATAPTEAAQIISAA GDTLSVPAPAVQPEESLKT DHP EIGEKGPTPALSEEASSSIRERP PEEVAAARLAQQEKQEQVKIESL AKSLEDALRQTASVTLQAIQAAQ NAAVQAVNAHSNLIKAAAMDNS EIAGEKKSQAQWRTVEGALKER RKAVDEAADALLKAK*LLMDF NKEELEKMKSVIENAKKKEVA GAKPHITAAEGKLHNMIVDLD NVVKKVQAAQSEAKVVSQYH ELVVQARDDFKRELD SITPEVL PGWKGMVSVDLADKLSTDDL N SLIAHAHRRIDQLNRELAEQKA TEKHITLAL/EKQKL/EEKRAF/ DSAVAKAFNRHRRKLKYRA*TG QKR*KEVRDAME/NEMRTQLR RQAAAHTDHLRDVLRVQEQEL KSEFEQNLSEKLSEQLQFRRLS QEQVDNFTLDINTAYARLRGIE QAVQSHAVAEERARKAHQLW LSVEALKYSMTSSAETTSIPL GSAV/EATKANCSDNFTQALT AATP/PESLTRGVVTVKRPLGAR FYAVQKLARRVAMIDETRNSL YQYFLSYLQSLLLFPFQQLKPPP
15408	45776	A	15498	1	1212	MPKKRQALVEFEDVLGACNAV NYAADNQIYIAGHPAFVNYSTS QKISRPGDSDSRVNSVLLFTI LNPIYSITTPRLNVFKNDQDT WDYTNPNLSGGQDGPSPNKR QRQPPLLGDHPAEYGGPHGGY HSHYHDEGYGPPPPHYEGRRM GPPVGEYGPADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVE KVKISLKKQSPGGRPMGEEWL/ DGYAVDRAITHLNNFMFGQK LNV/CVGAQAREGSRGTGERK GGEWGPAEEHSEAEVLTHTM GCGSVSKQPAIMPQSYGLEDG SCSYKDFSESRRNRFTPEQAA KNRIQHPNSVLHFFNAPLEVTE ENFFEICDELGVKRPSSVKVFSG KSERSSSGLLEWESKSDALET LFLNHYQMKNPNSINLVT

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15409	45777	A	15499	1	645	
15410	45778	A	15500	3	677	SPPNPRAPYLFPASLQNPANWS PHFYQLPILSQPRSVLTAFRQQA QPRISMPQAQTPFRPQMERLDQ NIRRSNQPHSLKPKLIQSKALT LFNSVKAEEKDEEAEEKFEVTR VVHIRGLIDGVVEADIVEALQE FGLISYVMVMSKKRQALVEFE DVLACNAVNYTADNQIHIAH HPAFVNYSTQKISRPGNSDDIR SVNSVLLFTILNPIYSITTDVLYT
15411	45779	A	15501	2	1712	DEQRRRSGAMVKMAAAGGGG GGGRYYGGGSEGGRAPKRLKT DNAGDQHGSGGGGGGGAGAA GGGGGGENYDDPHKTPASPVV HIRGLIDGVVEADLVEALQEFQ PISYVVVMPKKRQSLV*FEDVL GAGNAVNYAADNQIYIAGHPA FVNYSTQKISRPGSDSDSRVS NSVLLFTILNPIYSITTDVLYT CNPCGPVQRIVIFRKNGVQAMV EFDSVQSAQAKASLNGADIYS GCCTLKIEYAKPTRLNVFNQNDQ DTWDYTNPNLSSGQDGPSSNP KRQRQPPLLDGHPAEYGGPHG GYHSHYHDEGYGPPPHYEGR RMGPPVGGHRRGPSRYGPQYG HPPPPPPPEYGPHADSPVLMV YGLDQSKMNGDRVFNVCLYG NVEKVKFMKSKPGAAMVEMA DGYAVDRAITHLNNFMFGQK LNVCSVKQPAIMPQSYGLED GSCSYKDFSESNNRFSPEQA AKNRIQHPSNVLHFFNAPLEV EENFFEICDELGVKRPSSVKVFS GKSERSSSGLLEWESKSDALET LGFLNHYQMKNPNGPYPYTLK
15412	45780	A	15502	1	528	NHQIRNDFITISPGVKADSRTSP PQQPASSFDITEAAVSFAKDSL GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP TQALNFTFKDKYKQIFLDGVDK RSQFWRYFAGNLASGGATGAT SLCFYYPPLDFAHTRVAADVKG AGAERELRGFGDCLVKIYKSDG IK
15413	45781	A	15503	1	1452	

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15414	45782	A	15504	2	991	RSAGVKGASRSPVLQQSASSF NMTDAAVSFAKDFLAGGVAA AISKTA VAPIERVKLL/LQVQ/H ASKQIAADKQYKGIIIGCVVRIP KEQGVLSFWRGNLANVIRYFPT QALNFAFKDKYKQIFLGGVDK RTQFWRYFARNLASGGAAGA TSLCFVYPLDFARTLAAADV GK AGAEREFRGLGDCLVKIYKSDG IKGLYQGFNVSVQGIIYRAAYF GIY/DTAG/MLPDPK/NTHIV/S WMIAQTVHCCCPG*LPYPFDT RS/VRRNE*MQSGRK/GT/DIMY TGTLDCWRKIARDEGGKAFFK GAWSNVLRGMGGAF/VLVLYE *KSKKYYT
15415	45783	A	15505	1	613	
15416	45784	A	15506	1	1695	
15417	45785	A	15507	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSA MEDEINEMKRE EKFREKRVRKNEQSLQEIWDYL KRPNLRLIGVPESDGENGTKE NTLQDIIQENFPNLARQANI/Q EIQRMPQRYSLRRATPRHII VRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL
15418	45786	A	15508	1	3156	
15419	45787	A	15509	1	879	
15420	45788	A	15510	1	804	
15421	45789	B	15511	1	1230	
15422	45790	A	15512	2	827	
15423	45791	A	15513	1	1011	
15424	45792	A	15514	1	1722	
15425	45793	B	15515	1	780	
15426	45794	A	15516	1	2712	
15427	45795	B	15517	1	855	

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15428	45796	A	15518	3	1263	GRTIQTGKGEVNFENFEKNLEECITRITNTEKCLKELMELKTKAREVREECSRSLRSCDQLEERVASAMEDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNRLRLIGVPESDVNGTKLENTLQDIIQENFNNLARQANVQIQERQRTQRYSSRRATPRHIIVRFTKVEMKEKMG LLVPNWNTNHSPLFRALFDYKGFRCRFGITHTGTGSPAGANQRGLAATLSGPGGEGQSAVARLTGLIGVPESDVKEKTKLETTLQDIIQENFPILARQANVQIQEIQRTPQRYSSRRATPRHIIVRFTKVEMKEKMLRAAREKGRVTLKGKPIRLTADLSAETLQARREWGPIFNILKEKNFQPRISYPAKLSFISEGEIKSFTDKQMLRDFVTTTRPALKELLKEALNMERNNRYQLQNHAK
15429	45797	A	15519	1	1137	
15430	45798	A	15520	1	1578	
15431	45799	A	15521	1	1656	
15432	45800	A	15522	1	1120	
15433	45801	B	15523	1	1541	
15434	45802	B	15524	1	1632	
15435	45803	C	15525	53	352	
15436	45804	A	15526	1	973	MGGKQNRKTGNSKMQSASPPP KERSSSPATEQSWMENDFDELREEGFRRSNYSELREDIQTGKKEVENFEKNLEECITRITNTEKCLKELMELKTKARELQRYSAMADEMNMKREGKFREKRIKRN EQSLQEIWDYVKRPNRLRLIGVPESDGNGTKLENTLQDIIQENFNNLARQANVQIQEIQRTPQRYSSRRATPRHIIVRFTKVEMKEKMLRAAREKGRVTLKGKPIRLTVDLSAETLQARREWGPIFNILKEKNFQPRISYPAKLSFISEGEIKYFTDKQMLRDFVTTTRPALQELLKEALNMERNNRYQLQNHAKM
15437	45805	A	15527	1	2896	
15438	45806	B	15528	50	658	
15439	45807	A	15529	1065	1260	RSHALALDSAGSSSPESH*RASIPHTALGQNAGSWAGTAHSHHGPFVWSDPRHPQVVPVHRTCCP
15440	45808	A	15530	96	219	EFSTKPRLSGP*SSWEMLEIPLAPDTTIDLKLLYSRDRF

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15441	45809	A	15531	5459	6324	LLANVSQLLADISQLLANFTQL FSHFSQLLTYLSKLFTHLPQLLT HFPKLLTHQPELFSNQSQLHPNI TRYSPSPSYSPSPSPNYTPTSPN YSPTSPSYSPSPSPSY/SDLTKLL PFQPTIHTVSNLYPKLTQLQPQ FAQLQPNLTQV/PPTSPSPSPSP EYTPTSPKYSPTSPKYSPTSPKY SPTSPTYSPTTPKYSPTSPYSIQ PLQSTPQPLPSTHLLAPLTRPLP PSTRPPAPPTRPPPKAQPTLPLP LVTRPPAPPTVSQARLSARMTV TRRTEGTWGAAAG
15442	45810	A	15532	13	941	SVVLRPLVVAAATATTPVAA AAANTAKKTATVMVGEMVA GERGVLQMGHDITRFFYSNIQT VINNWLLIEGHTIGIDSIADSK TYQDIQNTIKKAKQDVIETFEN QVPRILNDARDKTGSSAQKSL EYNNFKSMVVSAGKSKINISQ GGGSGGGRGGPPISMWLLALC LVGLAGAQRRGGGPGGGAPG GPGGLGLSLGEERFPVNTAYG RVRGVRRRELNNEILGPVVQFLG VPYATPPLGARRFQPEAPASW PGVRNATTLPPACQNLHGALP AIMLPVWFTDNLEAAATYGGC FRVPKKA
15443	45811	A	15533	207	696	TNLQEKNKQPHQKVGRYKQT LLKRRHLCSQQAHEKMLIITGH QRNANQHNHEIPSHTS*NGDH* KVRKQQLERMWRNRNRAFTL WVG*TSSTIVEDSMAIPQGR TRNTI*LSHPITGYIPKGL*IMLL *RHMHTYAYCGSIHNSKDLEPT QRSINDRLD
15444	45812	A	15534	1	307	
15445	45813	A	15535	1	381	LPPPHDRLWCVMFPTLCPSVLI VQFPMPSENMRCLVFPCNSLL RMMVSSFIHVPTKDMNSGIL*S RPADIELFSINLVNKKIFLKGF GDPLSLQRQLRNIVFSMPCCFPS FLLPWVFSQLSVKPH
15446	45814	A	15536	134	278	DPAFLAPSPV/LMKQAPQATSG LMEPPGPSTPIVQRPRILLVIDD AHTD
15447	45815	B	15537	1	840	
15448	45816	C	15538	1	891	

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15449	45817	A	15539	1	3102	MYSHVITVCRHVKNKDILLNR QPTLHRPSIQAHRRARILPEEKVL RLHYANCKAYNADFDDGDEM AHFPQSELGRAEAYVLACTDQ QYLVPKDGQPLAGLIQDHMVS GASMTTRGCFFTREHYMELVY RGLTDKVGRVKLLSPSLKPFPL WTGKQHINRTKDKNHMIISIDA EKAFDKIQPFMLKTLNKLGD GTYLKIRAIYDKPTASIIINGQK LEAFPLKTGTRQGCPLSLFNI VLEVLARAIROEK
15450	45818	A	15540	1	779	IPMKDHDAIKLFIQIPRNLEDEK DLKPLFEFGKIYELTVLKDRFT GMHKGCAFLTYCERESALKAQ SALHEQKTLPGMNRPIQVKPAD SESREGDKKLFVGMNKQQSE DDVRR/LFEAFGNIEECTILRGP ERQTAKGCAFVKYSSHAEAAAG RPSTRLHGSQTMPGAFAVPVWV GQVSADTDKERTMR/RMQQMA GQMGMFNPMAIPFGAYGAYA QALMQQAALMASVAQGGYL NPMAAFAAAQMQMAALNM NGLAA
15451	45819	A	15541	1	1413	MEYYAAIKKDEFISFVGTWMK LETIILSKLSQMOKTKHRIFSLIV LCDITDILKEFTVAEAGGFALNE IMKEICKSRFSKVSLSHWKMW HSTASLGYHRVNVNTNPDPLNLC LGHCWLGRLDTGQKQACGGP GVCPGMFRACGNGAPCKEAP SVTEASSPDGSLCLGSHVPITP APLSSAQMVCHMVEDRRTVEL ILGATHNLFFSTPLTWSLRAIP GNCVLFLLKDYVTEPVRQSILHI AGPTFKQTPNLPFLKFPEATKA HGPNNVYQNDSTCEPTAQVSH WSSVSTLIASPVPGEDRKLFLV GMLNKQSQEDDVRR/LFEAFGN IEECTILRGPDGNSKARPLASSQ GAPSVKYSSHAEAAQAINALH GSQTMPLMQQAALMASVAQ GGYLNMAAFAAAQMQMAA LNPNGLAAAPMTPTQANGQP AAEENFANGIHPYPAQSPTAAD PLQQAAYAGVQYAGR

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15452	45820	A	15542	254	883	DLRKDSPWEHRQCCKREPGNS APPAPHSWGFAVFNPFRAGDVR QLCKRADTRTPSPRAPFGSAGA CRGCGRAGARSLASPKARTCIS SARRRAGGPLQLGAGSGQAKR PDR*TRREGANA*KTLHL/HSSL APSPGGVLAGFQEPGRPVAC CAATAAGGIRAGERR/PAAAAA AAPWAQKLRLRLQRRGPPGC R**MVSFPRLFSGTSTR
15453	45821	A	15543	1	768	MCDFGKSTSLPASPTSSANGR DNSTYRLKEQGGFMHSVASRD SCAESARYTDAHYAKSGYGAY TPSSYGANLAASLLEKEKLGFK PVPTSSFLTRPRTYGPFSSLLDYD RGRPLLRPDITGGGKRAESQTR GTERPLGSGLSGGSGFPYGVTN NCLSYLPINAYDQGVTLTQKLD SQSDLARDFSSLRTSDSYRIDPR NLGRSPMLARTRKELCTLQGL YQTASCPYLVLDYLENYGRKG SASQVPSQAPPSRVP

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15454	45822	A	15544	85	2249	SAEAMSGDGA TEQAAEYVPEK VKKA EKKLEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEIKAKNYDK GEKLFQRCLMKVLHIDLWKCY LSYVRETKGKLP SYKGKMAQ AYDFALDKIGMEIMSYQI WVD YINFLKGV EAVG SYAENQRITA VRRVYQRCGVNPMINIEQLWR DYNKYEEGINIH LAKKMIEDRS RDYMNARRVAKEYETVMKGL DRNAPSVPQNTQQAQQVDM WKKYIQWEKSNPLRTEDQTLIT KRVMFA YEQCLLVLGHPDIW YEAAYLEQSSKLLAEKGMN NAKLFSDEAANIYERAISTLLK KNMLLYFA YADYEESRMKYEK VHSIYNRLLAIEDIDPTLVYIQY MKFARRAEGIKSGRMIFKKARE DTRTRHHVYVTAALMEYYCSK DKSVAFKIFELGLKKYGDIP EY VLAYIDYLSHLNEDNNTRVLF E RVLTSGSLPPEKSGEIWARFLAF ESNIGDLASILKVEKRRTAFKE EYEGKETALLVD RYKFMDLYP CSASELKALGYKDVSRAKLAAI JPDVPVAPSIVPVLKDEVD RKP E YPKPD TQMIPFQPRHLAPGL HPVPGGVFPVPPAAVVL MKLLP PPICFQGPVQVDELMEIFRRCK JPNTEEA VRITTGAPELAVEG NGPVESNAVLTKA VCRPNEDS
15455	45823	A	15545	12	427	SAEAMSGDGA TEQAAEYVPEK VKKA EKKLEENPYDLDAWSIL IREAQV**YRITFPSLWVQSHYL VLPVNNIFIITL*MLFIGFQF*N QPIDKARKTYERLVAQFPSSGR FWKLYIEAEVTLFYFFLYQYCS IHL
15456	45824	A	15546	150	469	SAEAMSGDGA TEQAAEYVPEK VKKA EKELEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEVTLFYFIFS YISIAAFTVVIENKLG T
15457	45825	A	15547	1	834	
15458	45826	A	15548	443	732	SFMRWQKGQLPQLCLHRESHC SPYPQPSFLGMEPADIHETTFN SIMKCDVDIHKGLYANAVLSSG TTMYPGIA/NRMQKEITALAPS MMKIKIAPA

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15459	45827	A	15549	1	1214	MEEIEIALVIDNGSGMCKAGF AGDDAPRAVFPISVGRPRHQGV MVGMMQKDSYVVGDEAQSKRG ILTLKYPIEHGIVTNWDDMEKI WHHTFYNELRVAPEEHPVLLTE APLNPKANREKMTQIMFETNT PAMYVAIQAVLSLYASGRTTGI VMDSGGDVHTHTPIYEGYALP HAILRLDLAGRDLTDYLMKILT ERGSYFTTTAEREIVRDIKEKLC YVALDFEQEMATAAASSSSLEK SYELPDSRPSSTNWQLSGFRLPL RHSFQPSFLGMESCGMHETTF NSIMKCDVDIRKDLVANTVLS GRTPPCTLGADRMQKEITALA PSTMKIKIIPPERKYSVWIGGF HPWAWLSHLSKMWVQQARS MTESGPLHSSTANGFLGGLLTL VAFTPLWTKP
15460	45828	A	15550	1	2355	MKQITFAPRNLHLLTNTNTWTPD SQWL VDMRTSGASFTGETIER VNIPTGYVEKPNKQCRHSVTRY GHGGHSDHTPSLTATVATQIT PRHSGHSGHCDRNLSLATATA ATLITPHLLWPRWPLGSHSVT WCGHGGHSDHTPSPTTATAVT RITSRHPLRPQQSLGSHPVTHYS HGSHSDCIPVTRYAHGGHSDHT PSLAMATAATQMALCHSLWPR QPLGYLVNKIRRKRCTDGVSPS GKAPVFDTGIPWFESRYP SHLL RVSGSPPGYWGIAKRHQILNVS NMFQKFTNLLGYRQAVRHRI LIPAFRGSNPRTPANLFKTLTIS NMRALENDFFNSPPRKT VQFG GTVTEVLLKYKTAIEKRLEKLA VDPHRDRAQMLKVENVQQA W QQWINKLPARREDEDVKEIR WMIEELRVSYFAQQLGKNSRA ESMLWSFHKAIEAARTNIIQA QTRVEAAQATERRIAADIDDSE LKAPRDGRVQYRVAKPGEVLA AGGRVLNMVDLSDVYMTFFLP TEQAGTLKLGGEARLILDAAPD LRIPATISFVASVAQFTPKTVET SDERLKL MFRVKARIPPELLQ HLEYVKTGLPGVAWSFLYSINQ TICLRDLSIEAKLQALEATCKSL EEKLDLVTNKQHSPIQVPMVA GSPLRTTQMCKNVR/CVNP*AT VVPPVPVQPTTQQYQGLDAGA

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15461	45829	A	15551	1	956	MSSGRRDALARGLNSGDGAP HLGEHRQLEDVGGVTVTVTWT GRLQAAGCWTRSVSTAAAGR REPSTRDGAALSTEPPDPPERLG HRGSRAGLTALGHVTRGSSQ RGGRPPEWEHWLENGTRRTEL VDGVSYESWRRRPCRQGLER LVLENHVATDEDEPALKCQRL EINCQDPSIKSFLYSINQITICLR DSIEAKLQALEATCKSLEEKLD LVTNKHSPIQVPMVAGSPLRT TQMCNKVR/CAMHWLCVSCIF TCLPGWRPAAPDQGPAAISLCS LPSSSQGHREPLALGLPSALPPA HRQRLRGSATVPIPP
15462	45830	B	15552	161	925	
15463	45831	A	15553	31	856	GGFLHHASFFVGRGRTLLMYFS LLGATPKPEPEPEQVIKNYTEEL KVPPDEDICMEKLSAASGYS DVTDSKAVGPLAVGCLTKCSH AFHLLCLLAMYCNNGKGEHP NPGKPFRTARGFPAASATFTQTP GPQELVPYTPQITAWDLEGKVT ATTFSLQPRCVFDGLASTNDT VWLVAFAFNSASRGFQNPETLA DIPASQQLTDGHYMTLPVSPD QLPCDDPMAGSGGAPVLRVGH DHGCHQPPFCNAPLPGPGPYR WVVP TGALGLGLCLG
15464	45832	A	15554	827	1371	GSSAGEASSLRRLSPSQISRPL LPAGEKVLVVWIEDQTSNINPL SQQSKT/TLFNSMKAERGKEVT EEKLEARRGW/MRFKERSCFPN VKVQGEAANADIEAVACYPEY LAKITDEGGYTEQQIFSDETA LYWKKMPSTRFLARRKNCHSH PSFSSQHLVQSAAINIKAKSSTS KKIMTP
15465	45833	A	15555	799	906	FLNKLAFALRCGLALNSFLRKI QEPSLGSKSGSL
15466	45834	A	15556	143	560	

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15467	45835	A	15557	1059	1940	QQMQQEMRRKSKWMAMLGK WETYQNS/TKGHLMKRVYKGI PMNVRAEVWSVLLNIQEIKAK NPRQYRVMKEKGKRSSEIHQI DLAVSQTLRNHMFRRDRYGTK QQELFYLLAYSXNYPVVGVCYR DLSHIAALFLI.YLPEEDTFWAL VQLLASERHSCRVGEQLPLGLH AARPGDGHGPGPHLPVVASLL GAFRTSLLTPKEGTDPPPKS DAFHHPHQKASHPPRGCPCLPG ATPSGSDSVQLALRLNLRVLLPF SCSGSSCPWYPRKEALHPGGLE EQRLQLPLMGLVTG
15468	45836	A	15558	123	448	ALAAAVYPVSHSERTGEEAKKIC SVR*LLRSAQEEI/FLRGKNSRT GVL*KLLQRK*RYQRALGLAM LSEWTISPKGPVSTGITKPLMTA SRVTVPRMTMSALLDFIHGA
15469	45837	A	15559	1	6387	
15470	45838	A	15560	52	3218	
15471	45839	A	15561	3602	4015	GSVESPLGQKTPRTSSASPCWPS TNLYRMELEYGPHVTSQVVK STRCAPIRWSAAPSILCEVRVPV TMWTCLPLPATGRLSMW*IW RQWPCVLTSAATQS*LTRCGGGT RAVSLAPQSHL*VCPAQSSWTS IILWT
15472	45840	A	15562	932	1316	RVQDIPAKRGIPQFRPKIGIGQ SYKQHYPARPWNVLAQKVVV FEDQDALLPCLLTDPVLEAGVS LVRVVRGRPLMRHTNYSFSPWH GFTIHRAKFIQSQDYQCSALMG GRKVMISISIRLKVQKAVNRA
15473	45841	A	15563	1	263	
15474	45842	A	15564	66	185	
15475	45843	A	15565	1	4217	MRLAEERAALAAENADGEPGA DRRLRLLLGTYVAMSLRPAAGA WERCAGSAEAEQLLQAFGRD AAEGPRPLL.VVRGPRGLAIRP GLEVGPEAGLAGAKALFFLRGT PEPPGPDSEFRGAVVCGDLPAAP LEHLAALFSEVVLPLVLANEKNR LNWPHMICEDVRRHAHSLQCD LSVILEQVKGKTLPLPAGSEK MEFADSKSETVLDSIDKSVIYAI ESAVIKWSYQVQVVLKRESSQP LLQGENPTPKVELEF

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15476	45844	A	15566	26	494	RPGCGEVLGNAELWGQECQL HYSPVPSPWENSSGPRFSISKTG SLIPPLNDICQNKPKIILSHPA RCLGLLDHFPQQWERRQAQNR AETG*GQSAQGQTFRQRPLSV SGNCRVPPRATVSRK/PRPAPAY ALSLSKSPRRRPRTGTGPAPGLVP
15477	45845	A	15567	1	1242	
15478	45846	A	15568	114	1219	VDLPPGAPVRQSGSHGSVLRDH KTEGEARVPLHQRVVGKAGGR GATPGPHVHEDPVTICCGHSFC RP/C/ICLSWEEAQSPANCRA EPSQKKDFKTNILLKNLVTIAR KASLWQFLSSEKQICGTHRQTK KMFCDMDKSLCLLCSNSQEH GAHKHYPIEEAAEEHREKLLKQ MRILWKKIQENQRDLYEERT AFLWRKRTLRLKGMTSGAQGT SQKVALGLLQPLCHTVRAQS NSARVHKQRGGDAVSSGAGIP DPKAQRFPATLRSQAFTCTAGR RWGSGETVLHPLQRAGVRGAV AELHRQLLLSSAAAGFEECEGL CTSGPHITQGPDHQELYLSHEG VWTLFTCTGDRWKVLGSGVPCP

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15479	45847	A	15569	1	2694	MRMAATAWAGLQGPPPLTLCP AVRTGLYCRDQAHAEATDVV LLAPFCQPKTRSHGTCPPTERDP RGEGSTYVPRVDGIQGWGTR ALTGWTDRLLCQACQTLPPR HWFLPGARGWLGGSPCAHQGE SLPSQSPILLRVESVKSRMLRR RAQEEDSTVLIDVSPPEAEKRG SYGSTAHASEPGGQAAAAACRA GSPAKPRIADFLVWEEDLKLD RQQDSAAARDTDMHRTWRETF LDNLRAGLCVDQDDVDQGN TTVHYALLSASWAVLCYYAED LRLKLPLQDYPTPTPTGRPA/ CAWLGIPIVLLVVDVPPPEYY SCRFRVKNLPRFLGSDNQDTFF TSTKRHQLFEILAKTPYGHEKK NLLGIHQLLAEGVLSAFLHD GPFKTPPEGPOAPRLNQRQVLF QHWARWGKWNKYQPLDHVR RYFGEKVALYFAWLGFYTGWL LPAAVVGTLVFLVGCFLVFSDI PTQELCGSKDSFEMCPLCLDCP FWLLSSACALAQVREEAGRLF DHGGTVFFSLFMAWVALLLE YWKRSATLAYRWDCSDYED TEERPRQFAASAPMTAPNPITG EDEPYFPERSRARRMLAGSVVI VVMVAVVVMCLVSIILYRAIM AIVVSRSGNTLLAAWASRIASL TGSVVNLVFIILSKIYVSLAHV LTRWEMHRTQKFEDAFTLKV
15480	45848	A	15570	1	924	MISQIFENYFSGKSSATSGWA RAQRDRFVAGSARPAALLSGRL APPALGSERLSTRASSCGGLPR ATPRGRAPPAIRIIPVSTAQR LRSAAARQLLAGSSARGRDAL GKASWAPESVLEVLARAVRQE KEIKGILLGKEVKLSLFAQDMI VYLENPIISAQNLKLMSNFSK VSGYKISVQKSHAFVYTNNRQS ESQIMSELPFTVATKRIKYLGIQ LTRDVKDLFKENYKPLLNEIQE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTVFTE LEKTKFIWNQKRAHIAKTIL
15481	45849	A	15571	1	825	
15482	45850	A	15572	1	1488	

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15483	45851	A	15573	1	1476	MPIKVDWIKSRTHTPRDTMSP KRGINISIQEYRNTPDASILSEL LERDINTQVYTYEQEHTNKN GHQAIDKQNKGHIRRESDRGEY YPLDCRPTGSLTDKGWGMMLC GMMTAGKPTPILTLFDVGLPG GTAINKSSVIRVRNREEGNVEK WGERQVDQDAMVRVRCGIR NNVEAGLKYPGTMKVLSVF YTTQCCRRYLSVLCFAGLARAS VPFNEFDQMSLDEKLFSLHPL GSSSSPPKSLHCLLEHQFTML GFSDLGAQLASPSGSHTRAAGV AACQAPPTLTWLSPPVARGLG TLEQGVVLVGEARAAQEPMEW VGGSCMVGCRSRAALPRGKAAK AWREIQRASAGAGAPVSPWSG GAPSRACPPSASSVRFLCAARR LACNTYSPVLYCVRNWWILGL TDFNNEATDPRDFLANVPQGL AAVAIGTCGNNVYSAGDRDYR FALESILKACTLALEEVGPAA VQDKIGADP/TGLPF
15484	45852	A	15574	140	448	GFLGACAGREFKMAPP*SSLSG *KLSVSPCPGLLISAEGPEAVFSI V*NARVRGFILEVSETKNPPIDP TISTKHASLMSDSYREKKLVVPV VYPHSSSTPSFQ
15485	45853	A	15575	1	1001	MEAPQGALEQDGPVLSQQRH RKKPFTATPIDPSYHRSHALS VIIGYCVPPSHAAEMAAYGWT MGKSKLMAGQWITQSQVFCDS STDGPRQHKQAQTALTQLSQSQ RSTNNSTVSHRQQWVNCRLR VKCQRLRAHKELLVPQRWLWR QGRCPVTTSLVAVSETAGAGA AALALSRCLCLQVSASARPF SRTLSPQPKCWAMAASHQPIKG ILKNKTSRTSSMVALSEQPCRT VHEELSKKCQKWDEMNILSTY HPADKDYGLMKIDEPSPYHG\ LTGDDENACSDTETTETMVSDI LAKKLAAAEGLPEKYVWVQEQE SSGEEDLLAE
15486	45854	A	15576	1	1851	
15487	45855	A	15577	73	418	GKPDGDKVSHQLLLWKG/YSF/ PPSLMKLSLAGYEILS*KFFSLR TLNIGPPLSSGFRVSAERSTVSL MDFPLCITQCFSAPALNIFSIST LVNLTIMCLGVALLEQYLCCVL
15488	45856	A	15578	2	460	

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15489	45857	A	15579	1	2031	MATEVFLIPYALLQCSLASYPSP KPGIYVPSQPMWVGSVTCSDQ KNTIEVLVPKAYTLARQQYKSL SEQVYSCHQGTNLNTRAQESAAS LLKPARPRTRQKKETPNTSEHQ KEQTLDTPLRTVTLTRVRGFI LEVSETKNPPISDTMGLDISKQE EVLGRESDEQGEQSQGLSEMQ TALAMLLTREPISAKQAPHEPP RRQEDNTQAREGETRSRKTRA EGQKGHAHAENERNAKERESE RKRQEAEDENGKEKQERNEGT HARHMKRRKRDEKKRQGQNK PGNKRPEGNEEAQRRRKKNRE RQRFSEFYQSGPSAAGLLVFAGG PLQSLFAWVSPLEAAEQQRFLS VPSSGPLRKFCLYFGFVGNATP LRGLNTHGRLLTPAHGTRRRHT RPLNSPVPEKAGSTTESNGSPY GQNPGLPPKGNRAQGEKWM GRRIQGTTRPRAREANHKMT QIMFETNTPAVYMAIQAMLSL YTYGCTTGIVMDSSDGVTHITVP IYEGYALPRAILCLDVAGRDLT NYLMKILTEHSYSFTTMAEREI VCDIKEKLYYVTLDFEQEMAT AASSSSLEKSYELSDGQVITIGN ELSCCPEALFQPSFLSMESCDIH KTTFNSIMKCDMDIRKDLTYNT VLFGGNNMYPGIANRVQKIVTL VVMGSSILALLSTFQQMWVSK
15490	45858	A	15580	485	886	VPYFHFTCSHSSASQLPFLQMM KIAKTCSLGLNRLPEAKLKAFP TPRVTS/LWPRQGRPRR/GCGR NRSGSLVSAARGVGGRSQAAA ARRDAPSPPATSRMPPRQGSVS WGCARNAPGRRADPEVRRQPG PSCT
15491	45859	A	15581	1	435	
15492	45860	A	15582	2	339	HRCSTGAFSTAASNSNADRP ARRRGLPR/RGPP/SRRRSRPPR REPWPRTRRPRTRTAKARRRAT LEGRCCRACGHWPRAAAAAA AAAAAAVAAAAA GASATW

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15493	45861	A	15583	1067	2093	RRNTSSKCRSRNCRCPSPHRRH RPSLRPSRQPKCKCRPSRRSS RAPSSRRSRPQGLVPC*RAPPW PTSRWPGSPGFPLLNCSRKGRC RPRHPSQPRCPCSLRWCPSRQ LWSPHRESPPCP*TSRGSAAWRS VSIHRRQQDRPWWTQPVHMQQ LLKLLKQAAVQQQKAIQPAQAQ GPAAVQQKITAQQITTPGAQQK VAYAAQRALKNPVSYHTLPG PETGRGPASADPDGCKTSSSCS TANTRGQHPASCLCFPAGFSTD CGAHAGDGGRAAGADDPSCSDR DCPGGSAETHSAAGGDHGVGP APDSRRSQSPGARQLRQPKPA AQVTDEGPPCCQAKDITY
15494	45862	A	15584	10	607	RALCGESRLPLARKLS*AKKSV QRSTLQSRRIWVCWFHFAN*SL F*KQGR*ESPL*L*LIPAS*RPS TSESPL*KANFQQPHRGL*EKV AEGRRGP**EYVTSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSS SNSSNSRHRRRRRRRLSFLSR RRRHSRCCLSRSPRRRPRRHP ARLWLSRCTDQRKNFQLPRK TV
15495	45863	A	15585	217	1012	AKNDSKRQNFGRGQPTFGAD KAKGERVRTSSTIRTSYLDIT GPYLTGQWPRDPHGHPSCMK DKATQTPSCWAEEGAERSHQ RSAISWGSADQLKEETPTDLQ NAQQKLYKPEEVGCLISDFLKE KENCQPRILYAGKLSSECTPDE EAVNIVEMITKDEYYINLVDK EWQGLRGLTPILKEVLRVKCY QTASHATKSGMKGVQSFGK LHCYFKKLPLQLPSATAILISQ LTSTRQELHHKDCNLLKTQMI
15496	45864	A	15586	2	387	
15497	45865	A	15587	1	165	LFMFCCLLYIR*QLLHPGYNAPP QNTAATRGRGIAQTAEAAFL FLHQRVRFH
15498	45866	A	15588	172	359	PDGDGIESINYLGYGHFHDIDS SYP*AWNVLFPVCLFYFIEQWF IVLLEEVFHPICKLDS
15499	45867	B	15589	1	2850	
15500	45868	C	15590	1	2835	
15501	45869	C	15591	78	491	

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15502	45870	A	15592	1	5721	MAVLSLPLAPPTLMPPAHFNLV EMQVKATLKKEYWQRKSPGIPA GANRKKKINGSSPDATSGGYH SPGDSATGIYEGGHASSATLED LELRQPTPSTSPNDCSLVPSQS SSNSSSLHAPHSQYRELAVALH SSSAIISQLSENINSLNENKKSAL QLERQVKELKLGELKETVTS DP SNNGWEAVTSLWEGERLPARG AEEPRGSESTAAARPVPVSPAA VRGRLVAGEPGSYQPAETA AK AQLSLMALPGEY
15503	45871	C	15593	178	1287	
15504	45872	B	15594	52	855	
15505	45873	C	15595	1	1698	
15506	45874	A	15596	302	617	NLAVNPSGPGLFLIGKLLIASIS EHVIGLFRDSTSSWFLSRGVYV SRNLSVSSRFSLVFDDGDVQMG FWCGCPLCLLVFLTAGPSAA GLLEFAGGHLQTLFA
15507	45875	A	15597	1	2762	MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIGCDFSGTCRQ TLSILTQPLRQWGLEGIKKPNS WIIEESVSNGGPPLIPRQTAS GVDLQQTPTDLQRLVTVRRK TNKQKGIASSTKRTSTPKPHL YVTIHKDQSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWYDVYKRPDLRLIGVPD SDGENTRLNTLQDI
15508	45876	B	15598	1	1989	
15509	45877	B	15599	1	762	
15510	45878	A	15600	686	850	GQPERKVGLPTKGSPSD*QRISR QKLYKPKESGGQYSTFLKKRIF NPEFHIQPN
15511	45879	A	15601	2	382	
15512	45880	A	15602	1	993	
15513	45881	A	15603	3	460	SPCWGQLLQATQP/ATAFAQKD LLVGAVLFGHNGSLSSRNTLAF SMDVGPSQWMWGLLNGCGAS AHRQCTRCTLQVITALEGPLAP LKLAWHKKIYIFLGEAAEIRRD QLEAERELFHSRAEQGRFLVGR PGQAAHMLPPGDCVSIWTOH MIT
15514	45882	A	15604	1	130	
15515	45883	B	15605	1	561	

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15516	45884	A	15606	94	420	EKAVGRWIFQSKRYRSPCEKPY SKGLQVQRTVPEGPSKAAARA QAPGPNLLPCLPT/PQTPEFIIEP LANMYSCGNQNTLMELEAEQA QQHDEMLHMHALKEALSIIIS
15517	45885	B	15607	46	747	
15518	45886	A	15608	186	364	AFAPAPCTLVPGVLRGPPILLRE TGLAH*CPAVISPPKSLPWLPTA YVESQOVILFGL
15519	45887	A	15609	155	511	GAAVAGTQNLCLGGGAVGG S*RGALNGEGLHPGYNAFPQN TAATRDGRGIAQTAEAAQFLFL HQRVRFHC*FLLWREGRGR*AR REPLSRQPAPGLPGALPAPPL PDASTLVGVG
15520	45888	A	15610	1352	1684	MSIRSAWCRAEFNSWISLLTFC LVDLSLVFDDGDIQMGFWCCG PFCLLVFLTTAGPSAAGLLEFA GGPLQTLFAWASAVVAEEQOI LVSSKCCCLIVPLEVLSQRSTWP
15521	45889	A	15611	98	367	
15522	45890	A	15612	426	738	VCCVWGDPGPGAGHGEEAATL WKEKVDLKERVEKLELQFIHLS GQTDITGRKYISQGVASETQHW ERTTSSGWP*GPGGDEGEPA AGQVQLVGDHKEGKGK
15523	45891	B	15613	86	1411	
15524	45892	A	15614	950	1493	GTVFLWRRGTLIFRVSGFSAL FFPPSLWFYLPFVDDGDLQME FWYELSFLLMLLLFLCACWFSF *QSGPSAAGLLEFAGGPLQTLF AWVSAVAEEQWILVNRKCCC LIVPLEVLSQRSTRPCEVSVHPY VHCCLGIEELNIYCSLHSLGLFE AII.LGKAFELGCCDPSLFATV
15525	45893	A	15615	1	5731	MDSHRPTAWPAAVLAGRSPVA AESERYCSRQPLPRRQALLSV LVLASDTRLPPFWSSQTFCGILS KPLVLSGPLQTQGETNENGLV GGGEVGMQPLVLFERSLFPGR CVLERRIVPWMRQESYSSSSI WVDSDELNLTSVLECLEDDK NNNLLHQQLKWLICGLCRLYN LPKHLDVAMPDQPLPMGQSGP SAAGLLEFTGGPLQTLFAWVSA ALAAEKQILVNCKCCCLIVPLE VLSQRSTWQYELKEYW
15526	45894	A	15616	2	521	

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15527	45895	A	15617	1	1261	MSEHNITEECQQENQSQIEWRSI AHSDSIEVSWLHEVIKTYLKAK STKLDLMMKKL.KELSSQPSRKPK PFIPSQEGTGDNDVIYSTERLSK LLNQKKGSTRLYDKPLSNLLNQ KKVSTRTEGLIVDSRADMRNV TTILLSTESSSTDSSSSMDSSSM DSSSSIGRIVETATCAMIPVQKSK RSGPPQGPSAATGDGAEGRFLP RCSRWPADRLAWSQPRRLAP GPSAATGDGAEGRFPPLCSCCG TDRLAWPQPOGHLALLPRCGE CGRARELPDCCCLHAEGGCSSV LEVLAIRAIKQKEIEIQIGKQE VKLSLVADDIIFCLENATDSSRN LLELIKEFSKVSRYKINGHKSV LPYINSYQAENHIKNSTPFTIA TNNNNKK\KNLGIYLAKESKDS YNENYKTATERNHRWSQAR
15528	45896	B	15618	60	499	
15529	45897	A	15619	134	1416	RTSICWTMDSSVQNTVLGPTRS SVKGVMEWLQYLMERR/CTL SISMESMPRVAEDAGDVGAEE PLHLEPPAGPLEVEQQLQAEIK HLRKTLESALGQLAQVEANE GSSHLNRQQDERLREWKAELW EEQGETGRSSVQKDRTTISHAL SQNHQLEEQLAKEERLEATSQ NQQLQSQMSLMALPGEGDELG SKEEEEAPQMPMSILEDLKSREA MVAFLNSALVSAEEEEQQAQLH GQLKEQVRVCCQHLAHPVALAQ KEPEAAAPTPTGTGDSAVWTV DLQVEKTKFIMFTIKPGEVNVK DMAQSIYRSGKNLKDMDYGH DLEARRKTNRLPTFTFYFLSYE LDYSRCFIGCLKCLCLPSPATI GSFLKPSQKQKPVCLLYSLQNH EPIKPLFFINYPDSYSRYHTQVIR ILLSGSIHVQVPATKTPPL

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15530	45898	A	15620	1	1665	MGGHVGGGRHRLTPKLIPETL AAGSMKINPEEPNRPPINGAPG GPALPLAAGDSGSEQAGEPALA ASELQGWDSLGLSGPSLGRGTGI VATRSRSGRGLSPASLGRRSR DRKTKELAFAGSGLATRCQRA SSDAAGPPLSRCSPARTPQLPV RGLSLTGPRAPAPPRARVCLLSC SCRQPPPLTGGLNVGRPSGGS WKICPRSLPSASAEIGIRRRRAA AHPPLQPPPLCGESLPSVQCSA NADSSIPVPSRWQDACRNTGA AGPPGYPACVNNRNRDTKNSQ LDETHHMKTKVTDGRGGGAFT MLLRVVDGTHTSCSGSVEWDP RLYGDQADLSRSGHLDRPGA HDYYTAIKKCEEGSLDITTVK VKAGVNGFGRIEHLVTKPAFNS GKVDIVTINDPFVDLNNMVMY FQYDSTHGKFCGTVKAENRKL VASGNPITVFQ/ERDPSKIKWYI AESTCIFTTMEKAGADLQGGGA KRVIIAPSADAPMFVMDVNHE KYDNSLKIVSNASCITNCLAPL ANVIHNFIVGEGPMTTVHAIITA TQKIVDGPSPGKLA
15531	45899	A	15621	2	1105	GRVGCSTVSRIFSCVASRATSLR TPMGKVKVGVNGFGRIGRLVT RAAFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFGHTVK AENGKLVINGNPITTFQERVPS KIKWGDAGAEYFVESTGVFTT MEKAGAH\QGGAKRVIIAPS ADAPMFVMGVNHEKYDNSLKI ISNASCITNCLTPLAKVIHDF GIVEGLMTTVHAIATQKTLD GPSGKLWRDGRGAFQNIIPAS TGAAKAVGKVI* AERGLTGL MAFRVPTANVSVVDLTCRLEK PAKYDDIK\VKQGVGGPPQG AILGYTEH\QVVSDDCNSGPPV FPPFDAGVAGIALNDHFVKLISW YDNEFGYSNRVVDLMAHMAS
15532	45900	A	15622	121	221	
15533	45901	A	15623	189	538	

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15534	45902	A	15624	3	1015	DRAGPPGAPRLGQQLLCATILL GLAKKKEINITIIKQLKKFLN KKPSYGLERQMETTQNLVDSY MAIVNKTIVWDLVGVMPKTI MHVMINNTKEFISELLSNLYS RGDQKTLMEESAQAQWRDE MLRMYHVLKEALGIIIGDINTTI STVPWGPVDNSWLQVQSVLARR R/SPGLAPTAPSLPTPHRI.SLGA LGTGSVPTLLHHPGSSSVSSLSG LVA/DCFLPKARGGPGQRLPF PSLPGRLECDLAVAPPAPKAAP FICDFVYCCDQASEPVGCGQGT APHRLHGSGLIPQAPPQSIQA WLRAAVFWKALCPRCGRHIQ EFLHRTLVSL
15535	45903	A	15625	547	1242	PKALIKTSNKSLSYQLTTHSGT MACPWIRHEVLLSRLGFLVLEN TNMDKRPKLLRWLERQMETT QNLVDSYMAIVNKTIVWDLV GVMPKTIHVMINNTKEFISE LLSNLYSRGDQKTLMEESAQA AQRDEMLRMYHVLKEALGII GNINTTTISTVPWGPVDNSCLQV QSVLAGCSFILLVQAVFLLYQA WVLLFWAPQGERWPWTSGL DTVTRGEGSPKGLSISL
15536	45904	A	15626	108	308	AQKHHLT*LSFLPRH*ILT*NL KIPTS KIKKT PRSRPRSTSCFL DNLAPSCGCSGKSSWRIC
15537	45905	A	15627	687	1910	KDHQLRKKLRRRGKQGAFTAA LPPGSPRPLRGGRSGGVGLGV RGQRTQAPQAVTPSEGPEPLW GPVLGGGGEHRRGTGASAAAG ASMRRLLGAAGGGAGAGPQRG VGARVVVSEEA NSPGA AITSNR ETQDANEGLSAPRPECLLHPTC RLLYVPLIVRDWVCHTRSVVLL QVVNVGTGIAVGTGLASAYDTL MSQSFQVKNLKRVGILQRGVL ILMLCCFFCWADLVNTERILL LKQDPKSPGWTRCFQEWGSI HLVIPSMFMVCTEQWTFEIGNF LAGLIDVMEELGTQGIICELASV AYMNYFRLNPQPPISDFITNLAF LTLTERKILGYQLRKGPDIVGP YGLLQPFDTAVKFTKEPLWPS TSTITLYIAPTLALSHVLLALPT RMLAATPRPRGT
15538	45906	A	15628	1	1173	
15539	45907	A	15629	3	1447	

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15540	45908	A	15630	1	215	MDPKQEEIPDSPEKEFRRYRIAE WIRIHQPIICLQETHLTHKDSH KLKV/KGWNKAFHANGHQKSA ARETK
15541	45909	A	15631	1	1524	
15542	45910	A	15632	1	575	MALSERSQPQDHVSHDRIYVK HPEYANLYRQKVVDYTLPRVIS IHVGQAGVQIGNARWELCYCLE LAIQPDGQMPSDKTIGGGDDSF NMFFSEIGAGKHVPRAVFDLE PTVVDRCLGHWMAAFLGE/VEV HTGTYRQLFHPEQLISGKEDAA NNYSRGHYTIGK/EDLVLDRIH KLLTSQCRKPKATMWLSQAT
15543	45911	A	15633	208	465	
15544	45912	A	15634	107	827	EARRPCTLHLRSALHPATMCEL YSKRDTLGLRKKHIGPSCVKVF ASDPIKIVRAQRQYMFDENGEQ YLDGINNVAVHVGHCHEVVKAA ALKQMELLNTNSRFLHDNIVEY AKRLSATLPGETLCLLFYKFRG YWPSSNTNPSRPAAPASPPAAE RAGDFRAGRKPSVPGSRVSOGS PRGPCSRLSLSTFCTRYCPLSAL TSGPGCPYPMCFLLSPRVRLLY SSHMVAGCRALRRCKNSH
15545	45913	A	15635	3	1218	GGLWEKMAAAA\QSRVVRYLS MSRSAITA\ATSVCCHGPCCRQL HHALMPHGKGRSSVSIVAT VFGATGFLG\RYVVNHLGTAW GSQVIIP\YRV\IKY*QSMHLSFP WG*PGGQLSVFLGNWGTARD* RFLFRRVSYNTGNVGSILFGTR LGETKNF\DFWRDVFVKIPQAIA QLSKGSWEFEKFISCFHIWNGG II*KALS*DI*GNKAVGEKVVRD AFPEAIIIVKPSDIFGREDRFLNS FASMRHFGPIPLGLSLGWKT KQPVVYVDVSKGIVNAVKDPD ANGKSFAFVGPSRYLLFHLVK YIFAVAHRLLFPFLPLFAYRW VARVFEISPFEPWITRDKVERM HITDMKLPPLGLLEDLGQATP LELKAIEVLRHRRTYRWLSAEI EDVKPAKTVNI

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15546	45914	A	15636	2	799	GLWEKMAAAQSRVVRVLS\MSRSITAIAITSVCHGPPCRQLHHALMPHGKGGRSSVSGIVATGFGA\TGFLRRYV\VNHLGRMG SQVIIPYRC DKYDIMHLRPMGD LGQLLFLEW\DARDKDSIRRVV QHSNVVINLIGTRP\WKSNSD YEDVFVKIPQAI\AQLSK\EAG\VEKFIHV\SHLNANIKSSSRYLRNKNRKREKEEMKKDLLSKKEPE PEDLENSQLIHIAKNEKACFEENTKSVAEQPFDEEIVDATHQLTS YLGRSQE
15547	45915	A	15637	560	1394	RKSSSVHNAASGLGSRAPGAH RHLGRRCRCHRLVSPSPAMAE DL\SAATS\YTEDDFYCPVCQEV LKTPVRTTACQHVFCRCKFLTA MRESGAHCLPCRGNVTRRERA CPERALDLENIMR\KFGSGSRCC AK\QIKFYMRHHYKSKCKYQ DEYGVSSHPNFQISQDSVGNRIE NNTGIKQIPGAPFGDGRVVGCR QRNAKTELLAAAGESPCTMSL GSGPNLGPSPRSKSSSVTSPOPC FTEHPRERFVSFPVHYVLEGRS MSFLLWSLKTDRIFGH
15548	45916	A	15638	1	1026	MKVVCKEVKFEKQCP\EA\LLH WEQTDDDENKRC\DLREPRKPE THTKGPGLLVPTTQPGRNEGQS GADGKHARC\SKTS\CCLSGKEPS FIITEHCPLVPVQNTTIKPD\SGIR ILQTLDSRETFTMSTALDV\QM KEEDVLKFLAAGTHLGGTDLD FRMEQHICKRKSGGIYI\NLKRS WEKLLLVAPAIVA\IENPADVSV ISSSSTGQRAMLKCAAATGATP IAGHFTPGTFTNQI\QATFPNPRV LVVTD CRTGHQPLAEASYV\NN LPTIALCHTDSPLHHVDIA\PCN R\KAHSVDLMWMLAREILPMIR GTIARKHW\WEDPEEIEKEEQAAADKALTKEEFQGE
15549	45917	A	15639	20	441	TAEIAIPCNNKGAHSV\G*MWR MLAREDLRM\RGTS\GEHPWEV MPDLFYFYRDTEEIEKEEQAAAD KAVTKEEFQGEWTAPAPEFTAT QPEA\ADWSEGVQVPSVPIQ\QFP TEDWSAQ\ATEDWSA\PTAQAT EWVVGATT\DW
15550	45918	B	15640	88	531	
15551	45919	A	15641	1	1302	

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15552	45920	A	15642	150	957	KAGASCCGSANPYVSVGKSCV LLAMAQLQTRFYTDNKKYAVD DVPLSIPAASEIADLSNIINKLLK DKNEFHKHVEFDLIKGFRLRM PLDRHMEMENISSEEVVEIEYV EKYTAPQARSNAWFHDDWISSI KRGRGRILTGSYDKTSRIWSLE GKSIMTIVGHTDVVKDVAWVK KDSLSCLLSASMDQTILLWEW NVERNKVKALHCCCKGHAGSV NSIAVDGSGTKYFGLRIEPPKA VSLVEEINSLSYRWTADNYKV GSGGKEED
15553	45921	A	15643	3	393	VFCCPHCSLTFSKSFSSFSRLVR HQQTHWKQSYLCPICDLSFGE KEGLMD/HLEGL*RQGPQSSH HKCRVILQWLGFSDVPTMA GEEWKHGGDQSPRIHTPRRRG LREKACKGDKTKEA VSILKHK
15554	45922	A	15644	335	537	VYFKQVTLDSRCRL*ERQVKST SSWNILSSTWRLPFCPTSVVLR LTWICLRTITSSISWFPADSS
15555	45923	A	15645	153	828	

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15556	45924	A	15646	1	2002	MLESAGNQDIEDVDIVLRQIQV KNRSTTEVGQNGNLQVEVSYT QAHIAPRPLASQGTWPHFVSSA PQPCFQVQNHISKYQNLYYSGFI RETEPISKGDVGEWLSAGKGES SAMFASEQEISKDEQGTPLVGS FYWEVDSPRKESQAWAPGQE WIKLERDITTEKMFELKPIEP VQKTLPWVGEVAATLQEAMK RDCWREARVKKKPVTFEDVAV NFTQEEWDCLDASQRVLYQDVS MSETFKNLTSVEGKKKELREQ HPSLRDEGTSDDKVFLACRGA GQCPLSAPAGTMDRTRVLQAS QAGPP/FFATTVGKCFSSRSYL YSHQFVHNPKLTNSCSQCGKLF RSPKLSYHRRMHLGERPFCCT LCDKTYCDASGLSRHRRVHLG YRPHSCSVCGKSFDRDQSELKRH QKIHQNEPVDGNQECTLRIPG TQAEFQTPARSQRSIQGLLDVN HAPVARSQEPFIREGPMANQ ASVLKNQAPVTRTQAPITGTLC QDARSNSHPVKPSRLNVFCCPH CSLTFSKSKSYLSRHQKAHLTEP PNYCFHCKSFSSFSRLVRHQQ THWKQKSYLCPICDLSFGEKEG LMDHWRGYYKGKDLQSSHHK CRVILGQWLGFSHDVPTMAGE EWHGHDQSPPRJHTPRRRGLR EKACKGDKTKEAVSILKHK
15557	45925	A	15647	1	1048	MPSLAELFEGSSKAFGAAASQL NFPVASGEMLKFKYGLRNLPLH AVAAEPIASRTSRLNLFFQGGKPP FMTQQQMSPLSREGILDALFVL FEESQPALMKIKHVSNFVRKY SDTIAELQELQPSAKDFEVRSLV GCGHFAEVQVVRKATGDIYA MKVMKKKALLAQEQVSFFEEE RNILSRSTSPWIPQLQYAFQDK NHLVLMMEYQPGDLSLLNR YEDQLDENLIQFYLAELILAVH SVHLMGYVHRDIKPENILVDRT GHIKLVDFGSAKMNSNMVN AKLPIGTPDYMAPEVLTVMNG DGKGTGYLDCDWSVGVIAIY EMYGRSPFAEGTSARTFNNIM

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15558	45926	A	15648	101	220	KRQQAFLGLDLHQWFARGSQG FRLQTEGCIIGPPTFEV*RHSGFL SCQSSCTGSFSSVWADVPLMFE GAAQPV*PVPSRGADFRPLSIC *RSSRILLVKRCENSGVR
15559	45927	A	15649	597	808	ITMKSQRQIIKAVTTKEMKSV CRRD/TPAFMFIAALFKIAKIRIQ RLCLSTDEWIKKMWYIHTMEY YSTLK
15560	45928	B	15650	161	3156	
15561	45929	A	15651	14	270	
15562	45930	B	15652	787	1821	
15563	45931	A	15653	1	2412	MAKSKGCSAATLSTHQILVTP WSCDNQKCLQTLPNVPGGTLK LLCEDHWFRNDSCNQAIPAT LLSFPSLQASLWTTFLSPLNH HPVNPDSHLEQPPQSPRLNFE AGDPERAPHALGCKRSRTRTS DRQPMASRDPGWGKASVGGKA CALGSAVLPAGNDCTTDNLGL GSAGFEDLRLRLGQGP RRQGA LQAAPRKASSCAAGQRLAPDSS FSRKR RPSRQLGCEAAVADT AEAKSSEAPAFGWSTMDEAGS SASGGGFRALDEPPNSRIFLVI SKYTPESVLRERFSPFGDIQDIW VVRDKHTKESKGIAFVKFARSS QACRAM EEMHGQCLGPNDTKP IKVVRVPGSGCPRGKEWASWTS LHLLCRGEGGV EHPFPAADQT APGLGTGAALRRGSPPTKLRRV AGKGTGCGVFAPRERTROPRPP GDRTA VAGLPSPSPSLIHQLSS LPNSS*PTLSTFLTFLSQMPRFP YIKNGKTL/PFPQVFIAQSRSSGS HRDVEDEELTRIFVMIPKSYTEE DLREKFKVYGDIEYCSIKNKVT GESKGLGVYRYLKP SQAQAIE NCDRSFRILAEPKNKASESSE QDYYSNM RQALGHEPRVNMFM PFGHGVVQYFNVASAIYAKYK LHGFQYPPGNRIGVSFIDGNS ATEKMATQMVAAQLASMVVN NPSQQQFMQFGGSGSQLPQIQ

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15564	45932	A	15654	375	2059	DSSVWQTPQKQRAVRPLHSGG APWTKLAALRATRGFRPGVDS LDEPPNSRIFLVISKYTPESVLR RFSFPGDIQDIWVVRDKHTKES KGIAFVKFARSSQACRAMEEM HGQCLGPNDTKPIKVRVPGSGC PRGKEWASWTSLLHLLCRGEG GVEHPFAADQTAPGLGTGAA LRRGSPPTKLRRVAGKGTGCG VFAPRERTRQRPDPGDRATVAG LPLSLALTNPPELFTAKLVLA YFEYFSDLPLSDAQISYKKRKN STFPQVFIAQSRSSGSHRDVEDE ELTRIFVMIPKSYTEEDLREKFK VYGDIEYCSIIKNKVTGESKGL GYVRYLKPQAAQAIENCDRSF RAILAEPKNKASESSEQDYYSN MRQEALGHEPRVNMFPFGHGV VQYFNVASAIYAKYKLHGFQY PPGNRIGVSFIDGNSATDLLIK MATQMVAQ/RLHQWCGITQV SNNL/WQFGSGSSQLPQIQTD VVLPSCKKKAPAETPVKERLFI VFNPPLPLDVLEDIFCRFQNL EVYLVSGKNVGYAKYADRISA NDAIATLHWKDWSEWGET
15565	45933	A	15655	257	412	
15566	45934	A	15656	3	866	HAASPCCCYEKQSPQLQHLRV CSLRTWSLAARVAEGTAETVD PSAAPKTSVWSSRVCWGRLLA TISPSVNETDTCGMEDRRLVVC RPWRAQCHMKAWGWRHPPEEG GTHSGAPSAVLQALAVAIQLGG HLADPLLQVDPLSSCGAVSLDI LIYLVFYRTASVPETYIVKTLF KKLESQSLIQSNVLTSSNSMKA ERGEEAAKEKSEASRGWFMRF KERSCLHNIKMQGEAASADVE AAASYPKDLAKITDEHGYTKQ QFDVYKTAFCWRVLMKKYVK LLFVLCPLP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15567	45935	A	15657	333	1034	RLSTTVMRGAFFVFMHMKMPRL WLDYCCQFLMDQGRVTHTRRT FDRALRALPITQHSRIWPLYLRF LRSHPLPETAVRGYRRFLKLS ESAEEYIEYLKSSDRLDEAAQR LATVVNDERFVSKAGKSNYQL WHELCDLISQNPDKVQSLNVD AIIRGGLTRFTDQLGKLWCSLA DYYIRSGHFEKIRKAPVNGGPT WMVGQNSVPRFQTRRLTPLKR KGPLVTDFREKQPTPLAQE
15568	45936	A	15658	172	346	ARPCRWCPS*TSASAPGGLR PCPPAGGDRTPASPLHNQAAA APPGPTWRGAAAS
15569	45937	A	15659	293	482	
15570	45938	A	15660	468	791	LAKCGCLEARGRARQTSGRPRP TDGGP*SPCWETGKGHPVLGR RGS/PGKQGL*SLPQSCQGW CAASRLSSKNSWACMGSGREA VSQETGTSSSSLGLMRPSDKKP
15571	45939	A	15661	366	609	
15572	45940	B	15662	321	739	
15573	45941	A	15663	1	1815	
15574	45942	A	15664	1	1911	
15575	45943	A	15665	437	1125	PVSCSGHSRWAAAISIALSMIE TVNMVFTFYSRHHGTISTRVL/I GKRPERQDQDQTVNLGTLEET ASPSPVVTTSPQPMLPSAFPPL SEEINPALPEATVMASPEAVAR QDNVDSAQEPPTPLCASRPTT RQKSWWGARGEVESVTHEEM HYTGKELLEFSNL YKEKSGEQA WEWILRVVDNNGRNIQLDHPE FVDLGPLSRNSAFNAVVRGVK KGSKSLFAWLGEI
15576	45944	C	15666	49	186	
15577	45945	A	15667	80	877	GAERLPEPGPKRMVFRFVE/V GRVAYVSFGPHAGKI/VSAMVD VFIDQNKGFWSNGPCTQVR/RQ AVMPFKCMQLTDFILKFPHSAH QKYVRQSLGRREDINTKLQGP TRWQGRFESQEEKEKRLTDF *SVF**RAKEN*RDRIINPRNE V*EAFKRAAFPGKASSQKAPG Y*GVLLAAAAAAAAAAAAAA AAAAAAKIVPAKKITVAASKK APAQKVPAQK/ATGQK/AAAPAP KAQNGSKSKKQKAPAPKASG KESISGNHKK
15578	45946	A	15668	253	1218	
15579	45947	A	15669	1	1819	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
15580	45948	A	15670	1	2422	MCPILREHRGSTEGRKRRQKRLP LELTLKDEEVLAHREQIEVAKA SPSKGNIIHFYKGVYHDQQ DVTSNFLGAMWLISITFLSIGYG DMVPNTYCGKGVCLLTGIMGA GCTALVVAVVARKLELTKA EK HVVHFMMDTQLTKRHCPWAA TIQPKLSFLISLPGCDYRGESAR ARPLSHPPQLGLGKDARYLR CDRSLLCVCAAAGNAGLRPRD SPHTLLHWSRSPYFFSPKPVPP QLLGGQPAAHRRDDLGEAGV GRGGCCFAALRGVQSEKWSGF HTVPEPAPGQGDVMPVLVRPT NRRRLDSTGAGMGPSHHQQ ESPLPTITHCAGCTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPPP RSSHLHCQQQQSQDKPCPPFA PLPHPHHHPLAHQQPASGGSS PCLRCNSCASSGAPAAAGADNL SLLLRSTSSGGAFRTKTSPLSG SSCCCCSSRRGSQNLVSELTP SSHASALRQYYAQSAQQSAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHHHPAHHQH HQPARRESNPTEIAMSSCRY NGGVMRPLSNLSASRRNLHEM DSEAPQLQPPASVGGGGGASSP SAAAAAAA VSSAPEIVVSKP EHNNSNNLALYGTGGGGSTGG GGGGGSGHGSSSGTKSKKKK NQNIGYKLGHRRALFEKRRKLS
15581	45949	A	15671	1	246	SEPPHRRPTGALPSGAVRRGPL SSRPQIGRSTDSLHCVPKGATD AQRQP VKAAGSGAVPCKATG WSCP KL*EPISCINVTIC
15582	45950	B	15672	43	741	
15583	45951	A	15673	687	1012	FHTSRPFWNISELSRFICIQYKK PWHSVSDFYRYQFFICQGTACC PASLRM*HCPN*ILQGTSSQNCC SCSGKSCSPMQRRHRSTVCSGS GTFCVGSCESEFEGTYFSR